SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-1.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 1.rai.

<u>start</u>

Go Back to pre

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OM protein - protein search, using sw model

June 2, 2006, 19:12:07; Search time 12.7 Seconds Run on:

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-1

Perfect score: 76

Sequence: 1 QDYYEILGVSKTAEE 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents AA:* Database :

1: /EMC Celerra SIDS3/ptodata/2/iaa/5_COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description		
1	76 76	100.0	131 131	_	US-09-553-498-4 US-09-618-869-4	Sequence 4, Appli Sequence 4, Appli		

				_			
3	76	100.0	380	2	US-09-489-039A-9011	Sequence	9011, Ap
4	76	100.0	399	2	US-09-553-498-2	Sequence	2, Appli
5	76	100.0	399	2	US-09-618-869-2		2, Appli
6	63	82.9	375	2	US-09-328-352-4984	_	4984, Ap
				2	US-09-543-681A-5912	_	-
7	61	80.3	380				5912, Ap
8	60	78.9	87	2	US-09-882-835-4		4, Appli
9	58	76.3	372	2	US-09-270-767-45792	Sequence	45792, A
10	55	72.4	332	2	US-09-882-835-2	Sequence	2, Appli
11	55	72.4	373	2	US-09-710-279-890	_	890, App
12	55	72.4	385	2	US-09-134-001C-3688	-	3688, Ap
					US-09-198-452A-48		
13	55	72.4	392	2			48, Appl
14	55	72.4	406	2	US-09-438-185A-34		34, Appl
15	55	72.4	747	2	US-09-999-833A-459	Sequence	459, App
16	55	72.4	747	2	US-10-020-445A-459	Sequence	459, App
17	55	72.4	747	2	US-09-978-189-459	Sequence	459, App
18	55	72.4	747	2	US-10-017-085A-459		459, App
19	55	72.4	747	3	US-10-145-129A-459		459, App
20	55	72.4	747	3	US-10-013-929A-459	_	459, App
21	55	72.4	747	3	US-10-013-917A-459		459, App
22	54	71.1	376	3	US-10-375-010-22	Sequence	22, Appl
23	54	71.1	438	1	US-08-897-340-34	Sequence	34, Appl
24	54	71.1	438	2	US-09-252-329-34	-	34, Appl
25	54	71.1	484	1	US-08-879-260-4		4, Appli
26	54	71.1	484	2	US-09-231-529-4		4, Appli
27	54	71.1	484	2	US-08-977-816-4		4, Appli
28	54	71.1	484	2	US-09-639-207-5	Sequence	5, Appli
29	53	69.7	407	2	US-09-540-236-2899	Sequence	2899, Ap
30	52	68.4	411	2	US-10-101-464A-982		982, App
31	50	65.8	147	2	US-09-513-999C-6925	_	6925, Ap
32	50	65.8	368	2	US-09-861-451A-2		2, Appli
33	49	64.5	96	2	US-09-621-976-4045		4045, Ap
34	49	64.5	138	2	US-09-902-540-13689		13689, A
35	49	64.5	223	2	US-09-658-644-4	Sequence	4, Appli
36	49	64.5	223	2	US-09-949-016-6832	Sequence	6832, Ap
37	49	64.5	267	2	US-09-949-016-11497	Sequence	11497, A
38	49	64.5	387	2	US-09-908-992B-11		11, Appl
39	49	64.5	414	2	US-09-908-992B-10	-	10, Appl
					US-09-908-992B-9		
40	49	64.5	453	2			9, Appli
41	49	64.5	453	2	US-09-908-992B-30		30, Appl
42	49	64.5	480	2	US-09-908-992B-8		8, Appli
43	49	64.5	480	2	US-09-908-992B-12	Sequence	12, Appl
44	48	63.2	276	2	US-09-270-767-43364	Sequence	43364, A
45	48	63.2	381	2	US-09-252-991A-27174		27174, A
46	48	63.2	419	1	US-08-686-417-3	=	3, Appli
47	48	63.2	504	2	US-09-231-529-6		6, Appli
48	48	63.2	504	2	US-08-977-816-6		6, Appli
49	48	63.2	516	2	US-09-949-016-9654		9654, Ap
50	47	61.8	138	2	US-09-270-767-42296	Sequence	42296, A
51	47	61.8	382	2	US-09-603-208A-40	Sequence	40, Appl
52	47	61.8	452	2	US-09-908-992B-29	Sequence	29, Appl
53	47	61.8	479	2	US-09-908-992B-28		28, Appl
54	47	61.8	508	2	US-09-639-207-1		1, Appli
55	46	60.5	288	2	US-09-540-236-2885		2885, Ap
56	46	60.5	330	1	US-08-868-288A-3		3, Appli
57	46	60.5	330	2	US-09-235-373-3	-	3, Appli
58	46	60.5	330	2	US-09-388-993-3	Sequence	3, Appli
59	46	60.5	330	2	US-09-501-714-3		3, Appli
60	45	59.2	348	1	US-08-974-546-1		1, Appli
61	44	57.9	70	2	US-09-621-976-4403		4403, Ap
62	44	57.9	595	2	US-10-104-047-2714		2714, Ap
63	43	56.6	153	2	US-09-621-976-5129	sequence	5129, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-1.ra

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 1.rapbm.

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OM protein - protein search, using sw model

June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

US-10-001-938-1 Title:

Perfect score: 76

Sequence: 1 QDYYEILGVSKTAEE 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2097797 segs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA Main:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query No. Score Match Length DB					ID Description			
1 2	76 76	100.0	_		US-10-001-938-1 US-10-369-493-689	Sequence 1, Appli Sequence 689, App		
3	76	100.0	•	_	US-11-080-458-32	Sequence 32, Appl		

4	68	89.5	378	4	US-10-369-493-386	-	386, App
5	67	88.2	476	5	US-10-450-763-48130	Sequence	48130, A
6	62	81.6	370	6	US-11-097-143-5622	Sequence	5622, Ap
7	61	80.3	332	4	US-10-369-493-2834	Sequence	2834, Ap
8	60	78.9	87	4	US-10-145-586-48	_	48, Appl
9	60	78.9	378	4	US-10-369-493-21305	_	21305, A
10	58	76.3	372	4	US-10-369-493-23206		23206, A
						-	
11	58	76.3	382	4	US-10-369-493-8065	_	8065, Ap
12	58	76.3	385	4	US-10-369-493-16754	-	16754, A
13	57	75.0	187	4	US-10-424-599-165088	Sequence	
14	57	75.0	201	5	US-10-732-923-9541	Sequence	9541, Ap
15	57	75.0	288	4	US-10-369-493-8874	Sequence	8874, Ap
16	57	75.0	322	4	US-10-369-493-20073	Sequence	20073, A
17	57	75.0	367	4	US-10-369-493-8095	Seguence	8095, Ap
18	56	73.7	317	4	US-10-156-761-14768	_	14768, A
19	56	73.7	330	4	US-10-369-493-18826	-	18826, A
20	56	73.7	330	4	US-10-369-493-19832	_	19832, A
21	56	73.7	377	6	US-11-045-004-1504		1504, Ap
22		73.7	420	4	US-10-369-493-591	-	591, App
	56						
23	56	73.7	420	4	US-10-767-701-46164		46164, A
24	56	73.7	422	4	US-10-425-115-332061	Sequence	
25	56	73.7	427	4	US-10-424-599-282287	Sequence	
26	56	73.7	429	4	US-10-425-115-209640	Sequence	
27	56	73.7	429	6	US-11-096-568A-18416		18416, A
28	56	73.7	433	4	US-10-425-114-63266		63266, A
29	56	73.7	435	4	US-10-425-114-59462	Sequence	59462, A
30	56	73.7	435	4	US-10-425-114-65366	Sequence	65366, A
31	56	73.7	485	4	US-10-369-493-12487	Sequence	12487, A
32	55	72.4	110	3	US-09-764-868-1151	-	1151, Ap
33	55	72.4	157	3	US-09-764-868-778	_	778, App
34	55	72.4	208	4	US-10-767-701-41491		41491, A
35	55	72.4	308	4	US-10-369-493-19014	_	19014, A
36	55	72.4	319	4	US-10-282-122A-68006	_	68006, A
37	55	72.4	332	4	US-10-145-586-46	-	46, Appl
				4			9305, Ap
38	55	72.4	362	_	US-10-369-493-9305		
39	55	72.4	373	5	US-10-793-626-890	-	890, App
40	55	72.4	374	6	US-11-098-686-10930	_	10930, A
41	55	72.4	379	4	US-10-369-493-7330	_	7330, Ap
42	55	72.4	380	4	US-10-369-493-4573	•	4573, Ap
43	55	72.4	392	4	US-10-289-762-48		48, Appl
44	55	72.4	420	4	US-10-437-963-128712	Sequence	128712,
45	55	72.4	747	3	US-09-978-295A-459	Sequence	459, App
46	55	72.4	747	3	US-09-938-418-9	Sequence	9, Appli
47	55	72.4	747	3	US-09-978-697-459	Sequence	459, App
48	55	72.4	747	3	US-09-978-192A-459	Sequence	459, App
49	55	72.4	747	3	US-09-999-832A-459	Sequence	459, App
50	55	72.4	747	3	US-09-978-189-459		459, App
51	55	72.4	747	3	US-09-978-608A-459		459, App
52	55	72.4	747	3	US-09-978-585A-459		459, App
53	55	72.4	747	3	US-09-978-191A-459		459, App
54	55	72.4	747	3	US-09-978-403A-459	-	459, App
		72.4	747	3	US-09-978-564A-459		459, App
55	55						
56	55	72.4	747	3	US-09-999-833A-459		459, App
57	55	72.4	747	3	US-09-981-915A-459		459, App
58	55	72.4	747	3	US-09-978-824-459	_	459, App
59	55	72.4	747	3	US-09-918-585A-459	-	459, App
60	55	72.4	747	3	US-09-999-834A-459		459, App
61	55	72.4	747	3	US-09-978-423A-459		459, App
62	55	72.4	747	3	US-09-978-193A-459		459, App
63	55	72.4	747	3	US-09-999-830A-459	_	459, App
64	55	72.4	747	3	US-09-978-757A-459	Sequence	459, App

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-1.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

58871

Title:

US-10-001-938-1

Perfect score: 76

Sequence: 1

1 QDYYEILGVSKTAEE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11 NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

•							
	No.	Score	Match	Length	DB	ID	Description
_	1	76	100.0	15	 6	US-10-490-949-2	Sequence 2, Appli
	2	58	76.3	367	6	US-10-953-349-1406	
	3	58	76.3	456	6	US-10-953-349-1405	Sequence 1406, Ap Sequence 1405, Ap
	4	52	68.4	420	6	US-10-953-349-13709	
	5	50	65.8	380	6	US-10-953-349-7175	Sequence 13709, A
	6	50	65.8	389	7		Sequence 7175, Ap
	7	50	65.8	389	7	US-11-122-986-185	Sequence 185, App
	8	50	65.8	391	6	US-11-122-986-187	Sequence 187, App
	9	50	65.8	417	6	US-10-953-349-7174 US-10-953-349-16377	Sequence 7174, Ap
	10	50	65.8	442	6		Sequence 16377, A
	11	49	64.5	465	6	US-10-953-349-7173	Sequence 7173, Ap
	12	49	64.5	473	6	US-10-953-349-8070	Sequence 8070, Ap
	13	49	64.5	473	6	US-10-953-349-8069	Sequence 8069, Ap
	13 14	48		504	6	US-10-953-349-8068	Sequence 8068, Ap
			63.2			US-10-511-937-2547	Sequence 2547, Ap
	15 16	47 46	61.8 60.5	391 419	6	US-10-953-349-7627	Sequence 7627, Ap
	17				6	US-10-953-349-1054	Sequence 1054, Ap
	18	43 42	56.6 55.3	379 336	6 6	US-10-953-349-11645	Sequence 11645, A
	19	42	55.3	430	6	US-10-953-349-33810	Sequence 33810, A
	20	41	53.9	199	6	US-10-953-349-33809	Sequence 33809, A
	21	41				US-10-953-349-9116	Sequence 9116, Ap
	22	41	53.9 53.9	248 273	6 6	US-10-953-349-9115 US-10-953-349-4464	Sequence 9115, Ap
	23	41	53.9	349	6	US-10-953-349-948	Sequence 4464, Ap
	24	41	53.9		6		Sequence 948, App
	25	41	53.9	349 367	6	US-10-953-349-4463	Sequence 4463, Ap
	26			15	6	US-10-953-349-4462	Sequence 4462, Ap
	27	40 39	52.6 51.3	305	6	US-10-490-949-19 US-10-953-349-23847	Sequence 19, Appl
	28	39	51.3	583		US-10-953-349-25647 US-10-953-349-35418	Sequence 23847, A
	29	39	51.3	630	6 6	US-10-953-349-35417	Sequence 35418, A
	30	39	51.3	750	6	US-10-533-349-33417 US-10-511-937-2413	Sequence 35417, A
	31	38	50.0	333	6	US-10-951-957-2415 US-10-953-349-2863	Sequence 2413, Ap Sequence 2863, Ap
	32	38	50.0	333	6	US-10-953-349-2863	_
	33	38	50.0	397	7	US-11-293-697-3837	Sequence 11247, A Sequence 3837, Ap
	34	38	50.0	426	7	US-11-293-697-4751	Sequence 4751, Ap
	35	37	48.7		6	US-10-490-949-20	Sequence 20, Appl
	36	37	48.7	95	6	US-10-953-349-31080	Sequence 31080, A
	37	37	48.7	156	6	US-10-953-349-5018	Sequence 5018, Ap
	38	37	48.7	365	7	US-11-180-275A-5	Sequence 5, Appli
	39	37	48.7	408	6	US-10-953-349-32513	Sequence 32513, A
	40	37	48.7	496	6	US-10-953-349-32512	Sequence 32512, A
	41	37	48.7	524	6	US-10-953-349-32511	Sequence 32511, A
	42	36	47.4	15	6	US-10-490-949-18	Sequence 18, Appl
	43	35.5	46.7	283	6	US-10-953-349-23347	Sequence 23347, A
	44	35.5	46.7	301	6	US-10-953-349-23346	Sequence 23346, A
	45	35.5	46.7	353	6	US-10-953-349-23345	Sequence 23345, A
	46	35	46.1	253	6	US-10-953-349-5910	Sequence 5910, Ap
	47	35	46.1	260	7	US-11-293-697-2489	Sequence 2489, Ap
	48	35	46.1	268	6	US-10-953-349-5909	Sequence 5909, Ap
	49	35	46.1	277	6	US-10-953-349-24470	Sequence 24470, A
	50	35	46.1	292	6	US-10-953-349-24469	Sequence 24469, A
	51	35	46.1	300	6	US-10-953-349-24468	Sequence 24468, A
	52	35	46.1	302	6	US-10-953-349-5908	Sequence 5908, Ap
	53	35	46.1	332	7	US-11-297-134-48	Sequence 48, Appl
	54	35	46.1	335	6	US-10-953-349-2182	Sequence 2182, Ap
	55	35	46.1	339	6	US-10-953-349-12422	Sequence 12422, A
	56	35	46.1	343	6	US-10-953-349-2181	Sequence 2181, Ap
	57	35	46.1	431	6	US-10-953-349-22612	Sequence 22612, A
	58	35	46.1	557	7	US-11-293-697-4833	Sequence 4833, Ap
	59	34	44.7	138	6	US-10-953-349-25278	Sequence 25278, A
							•

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-10

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 10.rai.

start

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:12:07; Search time 12.7 Seconds

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-10

Perfect score: 78

Sequence: 1 KDYYQTLGLARGASD 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length I	DВ	ID	Description		
1	78	100.0	340	1	US-08-974-546-5	Sequence 5, Appli		
2	78	100.0	340	2	US-09-949-016-6691	Sequence 6691, Ap		

_	7.0	100 0	262	_	00 040 016 0000	_	
3	78	100.0	363	2	US-09-949-016-8899	Sequence	-
4	56	71.8	138	2	US-09-270-767-42296	Sequence	
5	56	71.8	508	2	US-09-639-207-1	Sequence	1, Appli
6	54	69.2	334	3	US-10-429-223-3	Sequence	3, Appli
7	54	69.2	337	2	US-09-665-479A-8	Sequence	8, Appli
8	52	66.7	391	2	US-09-902-540-11110	Sequence	
9	51	65.4	381	2	US-09-252-991A-27174	Sequence	•
10	50	64.1	364	2	US-09-270-767-43685	Sequence	
	50	64.1					
11			375	2	US-09-328-352-4984	Sequence	
12	50	64.1	376	3	US-10-375-010-22	Sequence	
13	48	61.5	147	2	US-09-513-999C-6925	Sequence	
14	48	61.5	348	1	US-08-974-546-1	Sequence	
15	48	61.5	387	2	US-09-908-992B-11	Sequence	
16	48	61.5	414	2	US-09-908-992B-10	Sequence	10, Appl
17	48	61.5	453	2	US-09-908-992B-9	Sequence	9, Appli
18	48	61.5	453	2	US-09-908-992B-30	Sequence	30, Appl
19	48	61.5	480	2	US-09-908-992B-8	Sequence	8, Appli
20	48	61.5	480	2	US-09-908-992B-12	Sequence	
21	47	60.3	452	2	US-09-908-992B-29	Sequence	
22	47	60.3	479	2	US-09-908-992B-28	Sequence	
23	47	60.3	554	2	US-09-167-299-4	Sequence	
24	46	59.0	372	2	US-09-270-767-45792	Sequence	
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25	46	59.0	438	1	US-08-897-340-34	Sequence	
26	46	59.0	438	2	US-09-252-329-34	Sequence	
27	46	59.0	484	1	US-08-879-260-4	Sequence	
28	46	59.0	484	2	US-09-231-529-4	Sequence	
29	46	59.0	484	2	US-08-977-816-4	Sequence	
30	46	59.0	484	2	US-09-639-207-5	Sequence	5, Appli
31	45	57.7	153	2	US-09-621-976-5129	Sequence	5129, Ap
32	45	57.7	276	2	US-09-270-767-43364	Sequence	43364, A
33	44	56.4	87	2	US-09-882-835-4	Sequence	4, Appli
34	43	55.1	261	2	US-09-902-540-15463	Sequence	
35	43	55.1	330	1	US-08-868-288A-3	Sequence	
36	43	55.1	330	2	US-09-235-373-3	Sequence	
37	43	55.1	330	2	US-09-388-993-3	Sequence	
38	43	55.1	330	2	US-09-501-714-3	Sequence	
39	43	55.1	373	2	US-09-710-279-890	Sequence	
	43		385	2	US-09-134-001C-3688		
40		55.1				Sequence	
41	43	55.1	395	2	US-09-712-363-164	Sequence	
42	43	55.1	493	2	US-09-613-303-19	Sequence	
43	43	55.1			US-10-267-311-19	Sequence	
44	42	53.8	130	2	US-09-252-991A-29173	Sequence	
45	42	53.8	320	2	US-09-328-352-7937	Sequence	_
46	41	52.6	70	2	US-09-621-976-4403	Sequence	
47	41	52.6	197	2	US-10-094-749-2714	Sequence	2714, Ap
48	41	52.6	358	1	US-08-868-288A-1	Sequence	1, Appli
49	41	52.6	358	2	US-09-235-373-1	Sequence	1, Appli
50	41	52.6	358	2	US-09-388-993-1	Sequence	1, Appli
51	41	52.6	358	2	US-09-991-181-148	Sequence	
52	41	52.6	358	2	US-09-501-714-1	Sequence	
53	41	52.6	358	2	US-09-990-444-148	Sequence	
54	41	52.6	358	2	US-09-997-333-148	Sequence	
55	41	52.6	358	2	US-09-992-598-148	Sequence	
					US-09-989-735-148		
56	41	52.6	358	2		Sequence	
57	41	52.6	358	3	US-09-989-726-148	Sequence	
58	41	52.6	358	3	US-09-997-514-148	Sequence	
59	41	52.6	358	3	US-09-989-728-148	Sequence	
60	41	52.6	358	3	US-09-997-349-148	Sequence	
61	41	52.6	358	3	US-09-997-653-148	Sequence	
62	41	52.6	358	3	US-09-989-293A-148	Sequence	
63	41	52.6	380	2	US-09-543-681A-5912	Sequence	5912, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 10.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 10.rapbm.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-10

Perfect score: 78

Sequence: 1 KDYYQTLGLARGASD 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA Main:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:* 6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용 Result Query No. Score Match Length DB ID Description ______ 78 100.0 1 15 4 US-10-001-938-10 Sequence 10, Appl

_				_		_	
2	78	100.0	70	6	US-11-047-063-1		1, Appli
3	78	100.0	340	4	US-10-116-275-134		134, App
4	78	100.0	340	4	US-10-116-275-135	_	135, App
5	78	100.0	340	5	US-10-871-388-5		5, Appli
6	78	100.0	340	5	US-10-792-571-16	Sequence	16, Appl
7	78	100.0	340	6	US-11-047-063-2	Sequence	2, Appli
8	78	100.0	377	5	US-10-450-763-48884	Sequence	48884, A
9	64	82.1	375	4	US-10-369-493-15859	Sequence	15859, A
10	64	82.1	376	4	US-10-369-493-15487	-	15487, A
11	63	80.8	258	3	US-09-764-868-1161	_	1161, Ap
12	63	80.8	387	4	US-10-408-765A-2002		2002, Ap
13	59	75.6	288	4	US-10-369-493-8874		8874, Ap
14	56	71.8	344	6	US-11-087-099-977		977, App
15	56	71.8	474	4	US-10-437-963-139809	Sequence	
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16	56	71.8	474	6	US-11-087-099-7037		7037, Ap
17	56	71.8	474	6	US-11-087-099-7585		7585, Ap
18	56	71.8	508	4	US-10-465-217-1		1, Appli
19	56	71.8	508	6	US-11-097-143-9177		9177, Ap
20	55	70.5	111	4	US-10-425-115-293770	Sequence	
21	55	70.5	203	4	US-10-425-114-60728	-	60728, A
22	55	70.5	336	4	US-10-425-115-295968	Sequence	295968,
23	55	70.5	336	6	US-11-096-568A-20392	Sequence	20392, A
24	55	70.5	345	5	US-10-739-930-10685	Sequence	10685, A
25	55	70.5	371	4	US-10-425-114-47700	Sequence	47700, A
26	55	70.5	379	4	US-10-369-493-7330	-	7330, Ap
27	55	70.5	380	4	US-10-369-493-4573	_	4573, Ap
28	55	70.5	388	4	US-10-425-114-46994		46994, A
29	55	70.5	388	4	US-10-425-114-58689		58689, A
30	55	70.5	390	4	US-10-425-114-52134	_	52134, A
31	55	70.5	414	6	US-11-096-568A-20391		20391, A
32	54	69.2	158	4	US-10-425-114-48912		48912, A
33	54	69.2	193	3	US-09-925-301-983	-	983, App
34	54	69.2	326	4	US-10-425-115-300448	Sequence	
35	54	69.2	334	4	US-10-429-223-3	-	3, Appli
36	54	69.2	337	4	US-10-788-792-162		162, App
37	54	69.2	356	4	US-10-437-963-126176	Sequence	
38	54	69.2	378	4	US-10-369-493-8450	-	8450, Ap
39	52	66.7	310	4	US-10-369-493-4694	•	4694, Ap
40	52	66.7	329	4	US-10-282-122A-49700		49700, A
41	52	66.7	368	4	US-10-369-493-19421		19421, A
42	52	66.7	374	4	US-10-369-493-13658	Sequence	13658, A
43	51	65.4	88	4	US-10-425-115-294867	Sequence	294867,
44	51	65.4	334	4	US-10-161-051-134	Sequence	134, App
45	51	65.4	334	6	US-11-097-143-22242	Sequence	22242, A
46	51	65.4	336	6	US-11-096-568A-25864	Sequence	25864, A
47	51	65.4	387	4	US-10-425-114-60791	_	60791, A
48	51	65.4	430	6	US-11-096-568A-25863	•	25863, A
49	51	65.4	513	6	US-11-097-143-11568		11568, A
50	50	64.1	332	4	US-10-369-493-2834		2834, Ap
51	50	64.1	342	6	US-11-097-143-3567	-	3567, Ap
52	50			_	US-11-097-143-15813		15813, A
		64.1	353	6		•	
53	50	64.1	362	4	US-10-369-493-9305		9305, Ap
54	50	64.1	365	4	US-10-369-493-18240		18240, A
55	50	64.1	370	6	US-11-097-143-5622		5622, Ap
56	50	64.1	376	4	US-10-375-010-22		22, Appl
57	50	64.1	376	6	US-11-232-406A-22		22, Appl
58	49	62.8	66	6	US-11-039-722-7		7, Appli
59	49	62.8	73	4	US-10-425-115-208567	Sequence	
60	49	62.8	128	6	US-11-097-143-15807		15807, A
61	49	62.8	271	6	US-11-087-099-7430		7430, Ap
62	49	62.8	317	4	US-10-156-761-14768	Sequence	14768, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-10.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds (without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-10

Perfect score: 78

Sequence:

1 KDYYQTLGLARGASD 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters:

58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description
1	78	100.0	15	6	US-10-490-949-19	Sequence 19, Appl
2	64	82.1	389	7	US-11-122-986-185	Sequence 185, App
3	64	82.1	389	7	US-11-122-986-187	Sequence 187, App
4	51	65.4	336	6	US-10-953-349-33810	Sequence 33810, A
5	51	65.4	430	6	US-10-953-349-33809	Sequence 33809, A
6	45	57.7	367	6	US-10-953-349-1406	Sequence 1406, Ap
7	45	57.7	456	6	US-10-953-349-1405	Sequence 1405, Ap
8	44	56.4	465	6	US-10-953-349-8070	Sequence 8070, Ap
9	44	56.4	473	6	US-10-953-349-8069	Sequence 8069, Ap
10	44	56.4	482	6	US-10-953-349-8068	Sequence 8068, Ap
11	42	53.8	273	6	US-10-953-349-4464	Sequence 4464, Ap
12	42	53.8	349	6	US-10-953-349-4463	Sequence 4463, Ap
13	42	53.8	367	6 6	US-10-953-349-4462	Sequence 4462, Ap
14 15	41 41	52.6 52.6	199 248	6	US-10-953-349-9116 US-10-953-349-9115	Sequence 9116, Ap
16	41	52.6	240	6	US-10-953-349-3115	Sequence 9115, Ap Sequence 18417, A
17	41	52.6	351	6	US-10-953-349-18416	Sequence 18416, A
18	41	52.6	504	6	US-10-533-345-10410	Sequence 2547, Ap
19	40	51.3	15	6	US-10-490-949-2	Sequence 2, Appli
20	40	51.3	260	7	US-11-293-697-2489	Sequence 2489, Ap
21	39	50.0	357	6	US-10-953-349-2656	Sequence 2656, Ap
22	39	50.0	364	6	US-10-953-349-2655	Sequence 2655, Ap
23	39	50.0	372	6	US-10-953-349-2654	Sequence 2654, Ap
24	39	50.0	380	6	US-10-953-349-7175	Sequence 7175, Ap
25	39	50.0	391	6	US-10-953-349-7174	Sequence 7174, Ap
26	39	50.0	442	6	US-10-953-349-7173	Sequence 7173, Ap
27	39	50.0	586	6	US-10-953-349-38530	Sequence 38530, A
28	39	50.0	627	6	US-10-953-349-38529	Sequence 38529, A
29	38	48.7	156	6	US-10-370-959-126	Sequence 126, App
30	38	48.7	169	6	US-10-953-349-27713	Sequence 27713, A
31	38	48.7	172	6	US-10-953-349-10393	Sequence 10393, A
32	38	48.7	324	6	US-10-953-349-10392	Sequence 10392, A
33	37	47.4	161	6	US-10-953-349-15793	Sequence 15793, A
34	37	47.4	182	6	US-10-953-349-15792	Sequence 15792, A
35 36	37	47.4	295	7 7	US-11-122-986-275	Sequence 275, App
36 37	37 37	47.4 47.4	295 417	6	US-11-122-986-277 US-10-953-349-16377	Sequence 277, App
38	37	47.4	420	6	US-10-953-349-16377 US-10-953-349-13709	Sequence 16377, A Sequence 13709, A
39	36	46.2	126	6	US-10-953-349-2572	Sequence 2572, Ap
40	36	46.2	188	6	US-10-953-349-17319	Sequence 17319, A
41	36	46.2	191	6	US-10-953-349-2571	Sequence 2571, Ap
42	36	46.2	230	6	US-10-953-349-2570	Sequence 2570, Ap
43	36	46.2	267	6	US-10-953-349-17318	Sequence 17318, A
44	36	46.2	310	6	US-10-953-349-21677	Sequence 21677, A
45	36	46.2	311	6	US-10-953-349-17317	Sequence 17317, A
46	36	46.2	311	6	US-10-953-349-21676	Sequence 21676, A
47	36	46.2	333	6	US-10-953-349-2863	Sequence 2863, Ap
48	36	46.2	333	6	US-10-953-349-11247	Sequence 11247, A
49	36	46.2	456	6	US-10-953-349-21675	Sequence 21675, A
50	35	44.9	317	6	US-10-953-349-11729	Sequence 11729, A
51	35	44.9	497	6	US-10-953-349-480	Sequence 480, App
52	35	44.9	498	6	US-10-953-349-479	Sequence 479, App
53	35	44.9	500	6	US-10-953-349-478	Sequence 478, App
54	34	43.6	95	6	US-10-953-349-31080	Sequence 31080, A
55	34	43.6	190	6	US-10-953-349-28214	Sequence 28214, A
56	34	43.6	191	6	US-10-953-349-28213	Sequence 28213, A
57 58	34 34	43.6	335	6	US-10-953-349-2182	Sequence 2182, Ap
58 59	34 34	43.6 43.6	343 344	6 6	US-10-953-349-2181	Sequence 2181, Ap
JJ	34	43.0	344	O	US-10-953-349-3691	Sequence 3691, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-11

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:37:25; Search time 14.6053 Seconds

(without alignments)

89.896 Million cell updates/sec

Title: US-10-001-938-11

Perfect score: 80

Sequence: 1 TTYYDVLGVKPNATQ 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description	
1	80	100.0	102	2	US-09-513-999C-5137	Sequence 5137, Ap	
2	80	100.0	127	2	US-09-370-838-199	Sequence 199, App	

3	80	100.0	127	2	US-09-854-133-199	Sequence	199, App
4	80	100.0	397	1	US-08-868-288A-5	Sequence	5, Appli
5	80	100.0	397	2	US-09-235-373-5	Sequence	5, Appli
6	80	100.0	397	2	US-09-388-993-5	Sequence	5, Appli
7	80	100.0	397	2	US-09-919-039-178		178, App
8	80	100.0	397	2	US-09-538-092-1052		1052, Ap
9	80	100.0	397	2	US-09-501-714-5		5, Appli
10	59	73.8		3			
			397		US-10-429-223-2		2, Appli
11	59	73.8	397	3	US-10-429-223-4		4, Appli
12	52	65.0	397	2	US-09-248-796A-17628		17628, A
13	51	63.7	482	2	US-09-538-092-454	Sequence	454, App
14	48	60.0	115	2	US-09-248-796A-16551	Sequence	16551, A
15	47	58.8	99	2	US-09-248-796A-19786	Sequence	19786, A
16	46	57.5	75	2	US-09-513-999C-6016	Sequence	6016, Ap
17	46	57.5	419	1	US-08-686-417-3		3, Appli
18	44	55.0	73	2	US-09-513-999C-7608		7608, Ap
19	44	55.0	96	2	US-09-621-976-4045	_	4045, Ap
20	44	55.0	223	2	US-09-658-644-4		4, Appli
21	44	55.0	223	2	US-09-949-016-6832		6832, Ap
22	44	55.0	267	2	US-09-949-016-11497		11497, A
23	44	55.0	382	2	US-09-603-208A-40		40, Appl
24							
	44	55.0	387	2	US-09-908-992B-11		11, Appl
25	44	55.0	414	2	US-09-908-992B-10		10, Appl
26	44	55.0	452	2	US-09-908-992B-29	_	29, Appl
27	44	55.0	453	2	US-09-908-992B-9		9, Appli
28	44	55.0	453	2	US-09-908-992B-30		30, Appl
29	44	55.0	479	2	US-09-908-992B-28	Sequence	28, Appl
30	44	55.0	480	2	US-09-908-992B-8	Sequence	8, Appli
31	44	55.0	480	2	US-09-908-992B-12	Sequence	12, Appl
32	43	53.8	158	2	US-09-248-796A-19793		19793, A
33	43	53.8	380	2	US-09-540-236-2987	Sequence	2987, Ap
34	43	53.8	504	2	US-09-231-529-6	-	6, Appli
35	43	53.8	504	2	US-08-977-816-6		6, Appli
36	43	53.8	515	2	US-09-248-796A-19787	_	19787, A
37	43	53.8	516	2	US-09-949-016-9654	_	9654, Ap
38	42	52.5	281	2	US-09-902-540-15871	-	15871, A
39	41	51.2	268	2	US-09-270-767-39827	-	
40	41			2			39827, A
		51.2	268		US-09-270-767-55044		55044, A
41	41	51.2	352	1	US-08-472-534-6	•	6, Appli
42	41	51.2	378	2	US-09-583-110-4647		4647, Ap
43	41	51.2	379	2	US-09-107-433-3487		3487, Ap
44	41	51.2	438	1	US-08-897-340-34		34, Appl
45	41	51.2	438	2	US-09-252-329-34		34, Appl
46	41	51.2	484	1	US-08-879-260-4	Sequence	4, Appli
47	41	51.2	484	2	US-09-231-529-4	Sequence	4, Appli
48	41	51.2	484	2	US-08-977-816-4	Sequence	4, Appli
49	41	51.2	484	2	US-09-639-207-5	Sequence	5, Appli
50	40	50.0	87	2	US-09-882-835-4		4, Appli
51	40	50.0	147	2	US-09-270-767-33311		33311, A
52	40	50.0	147	2	US-09-270-767-48528		48528, A
53	40	50.0	276	2	US-09-270-767-43364		43364, A
54	40	50.0	373	2	US-09-710-279-890		890, App
55	40	50.0	376	3	US-10-375-010-22	-	22, Appl
56	40	50.0	385	2	US-09-134-001C-3688	-	3688, Ap
57	40	50.0	400	2	US-09-134-001C-3888 US-09-489-039A-13012		13012, A
5 <i>7</i>						_	
	39	48.8	236	2	US-09-270-767-42239		42239, A
59 60	39	48.8	264	2	US-09-134-000C-6709	_	6709, Ap
60	39	48.8	284	3	US-09-191-651-10		10, Appl
61	39	48.8	320	2	US-09-543-681A-7884		7884, Ap
62	39	48.8	320	2	US-09-248-796A-17629		17629, A
63	39	48.8	330	1	US-08-868-288A-3	Sequence	3, Appli

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 11.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 11.rapbm.

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OM protein - protein search, using sw model

June 2, 2006, 19:58:51; Search time 63.3553 Seconds Run on:

(without alignments)

109.671 Million cell updates/sec

Title: US-10-001-938-11

Perfect score: 80

Sequence: 1 TTYYDVLGVKPNATQ 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications_AA_Main:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용 Result Query No. Score Match Length DB ID Description ______ 80 100.0 15 4 US-10-001-938-11 Sequence 11, Appl

_							
2	80	100.0	127	3	US-09-738-973-199	Sequence	199, App
3	80	100.0	127	3	US-09-854-133-199	Sequence	199, App
4	80	100.0	127	4	US-10-144-649A-199		199, App
5	80	100.0	397	3	US-09-919-039-178		178, App
6	80	100.0	397	5	US-10-473-127-1138	_	
							1138, Ap
7	80	100.0	397	5	US-10-473-127-1139		1139, Ap
8	80	100.0	397	5	US-10-473-127-1140	Sequence	1140, Ap
9	80	100.0	397	5	US-10-473-127-1143	Sequence	1143, Ap
10	80	100.0	397	5	US-10-473-127-1144	-	1144, Ap
11	80	100.0	397	5	US-10-473-127-1145	_	1145, Ap
	80			5		_	
12		100.0	397		US-10-756-149-4727		4727, Ap
13	80	100.0	397	5	US-10-631-467-559		559, App
14	80	100.0	397	5	US-10-631-467 - 1386	Sequence	1386, Ap
15	80	100.0	397	5	US-10-878-556A-155	Sequence	155, App
16	80	100.0	408	5	US-10-450-763-40099		40099, A
17	67	83.8	403	6	US-11-097-143-24405	_	24405, A
18	67	83.8	403	6	US-11-097-143-41904	_	
							41904, A
19	61	76.2	26	5	US-10-862-195-1870		1870, Ap
20	60	75.0	390	4	US-10-425-115-236372	Sequence	
21	60	75.0	391	4	US-10-767-701-45927	Sequence	45927, A
22	60	75.0	395	4	US-10-425-114-63467	Sequence	63467, A
23	60	75.0	398	6	US-11-096-568A-31579	_	31579, A
24	59	73.8	121	4	US-10-437-963-151256	-	
				_		Sequence	
25	59	73.8	313	4	US-10-437-963-183087	Sequence	
26	59	73.8	397	4	US-10-108-260A-3837		3837, Ap
27	59	73.8	397	4	US-10-429-223-2	Sequence	2, Appli
28	59	73.8	397	4	US-10-429-223-4	Sequence	4, Appli
29	59	73.8	426	4	US-10-108-260A-4751	-	4751, Ap
30	58	72.5	145	4	US-10-767-701-55698		55698, A
31	54	67.5	123	4	US-10-425-115-239628		
				_		Sequence	
32	53	66.2	51	4	US-10-424-599-274377	Sequence	
33	53	66.2	107	4	US-10-767-701-48835	Sequence	48835, A
34	53	66.2	208	4	US-10-767-701-41491	Sequence	41491, A
35	52	65.0	60	4	US-10-424-599-160806	Sequence	160806,
36	52	65.0	155	4	US-10-425-115-220433	Sequence	
37	52	65.0	217	4	US-10-424-599-271036	Sequence	
38	52	65.0	410	4	US-10-424-599-271035	-	
				-		Sequence	
39	52	65.0	417	4	US-10-424-599-271037	Sequence	
40	52	65.0	442	4	US-10-437-963-196211	Sequence	
41	51	63.7	212	4	US-10-425-115-309309	Sequence	
42	51	63.7	420	4	US-10-437-963-128712	Sequence	128712,
43	49	61.3	47	4	US-10-424-599-188229	Sequence	
44	49	61.3	80	4	US-10-424-599-205273	Sequence	
45	49	61.3	121	4	US-10-425-115-244815	Sequence	
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46	49	61.3	386	4	US-10-425-115-191974	Sequence	
47	49	61.3	391	4	US-10-425-114-63066		63066, A
48	49	61.3	391	4	US-10-425-114-63612	Sequence	63612, A
49	49	61.3	420	4	US-10-424-599-257607	Sequence	257607,
50	48	60.0	35	4	US-10-425-115-220432	Sequence	
51	48	60.0	64	4	US-10-424-599-247165	Sequence	
52	48	60.0	85	4	US-10-425-115-327744	•	
				_		Sequence	
53	48	60.0	94	4	US-10-425-115-336842	Sequence	
54	48	60.0	148	4	US-10-767-701-32479	_	32479, A
55	48	60.0	185	4	US-10-767-701-44451	Sequence	44451, A
56	48	60.0	195	6	US-11-096-568A-16365	Sequence	16365, A
57	48	60.0	197	4	US-10-425-114-61161		61161, A
58	48	60.0	200	4	US-10-425-115-298432	Sequence	
59	48	60.0	241	3	US-09-765-205-32		32, Appl
60	48	60.0	241	5			
					US-10-347-669-32		32, Appl
61	48	60.0	343	4	US-10-425-115-228357	Sequence	
62	48	60.0	344	4	US-10-425-114-73013	Sequence	73013, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-11.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:45:07; Search time 3.55263 Seconds

(without alignments)

48.831 Million cell updates/sec

Title:

US-10-001-938-11

Perfect score: 80

Sequence:

1 TTYYDVLGVKPNATQ 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters:

58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:* /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description
1	80	100.0	15	6	US-10-490-949-20	Sequence 20, Appl
2	59	73.8	397	7	US-11-293-697-3837	Sequence 3837, Ap
3	59	73.8	426	7	US-11-293-697-4751	Sequence 4751, Ap
4	57	71.2	379	6	US-10-953-349-11645	Sequence 11645, A
5	56	70.0	391	6	US-10-953-349-7627	Sequence 7627, Ap
6	49	61.3	420	6	US-10-953-349-13709	Sequence 13709, A
7	47	58.8	380	6	US-10-953-349-7175	Sequence 7175, Ap
8	47	58.8	391	6	US-10-953-349-7174	Sequence 7174, Ap
9	47	58.8	417	6	US-10-953-349-16377	Sequence 16377, A
10	47	58.8	442	6	US-10-953-349-7173	Sequence 7173, Ap
11	44	55.0	339	6	US-10-953-349-12422	Sequence 12422, A
12	43	53.8	190	6	US-10-953-349-28214	Sequence 28214, A
13	43	53.8	191	6	US-10-953-349-28213	Sequence 28213, A
14	43	53.8	504	6	US-10-511-937-2547	Sequence 2547, Ap
15	42	52.5	367	6	US-10-953-349-1406	Sequence 1406, Ap
16	42	52.5	456	6	US-10-953-349-1405	Sequence 1405, Ap
17	41	51.2 51.2	95	6 6	US-10-953-349-31080	Sequence 31080, A
18 19	41 41	51.2	333 333	6	US-10-953-349-2863 US-10-953-349-11247	Sequence 2863, Ap Sequence 11247, A
20	40	50.0	199	6	US-10-953-349-11247 US-10-953-349-9116	Sequence 9116, Ap
21	40	50.0	248	6	US-10-953-349-9115	Sequence 9115, Ap
22	40	50.0	548	6	US-10-953-349-17843	Sequence 17843, A
23	39	48.8	191	6	US-10-953-349-34839	Sequence 34839, A
24	39	48.8	193	6	US-10-953-349-34838	Sequence 34838, A
25	39	48.8	196	6	US-10-953-349-34837	Sequence 34837, A
26	39	48.8	198	6	US-10-953-349-31537	Sequence 31537, A
27	39	48.8	223	6	US-10-953-349-9541	Sequence 9541, Ap
28	39	48.8	226	6	US-10-953-349-9540	Sequence 9540, Ap
29	39	48.8	282	6	US-10-953-349-31536	Sequence 31536, A
30	39	48.8	331	6	US-10-953-349-31535	Sequence 31535, A
31	38	47.5	138	6	US-10-953-349-39107	Sequence 39107, A
32	38	47.5	156	6	US-10-953-349-5018	Sequence 5018, Ap
33	38	47.5	174	6	US-10-953-349-39106	Sequence 39106, A
34	38	47.5	583	6	US-10-953-349-35418	Sequence 35418, A
35	38	47.5	630	6	US-10-953-349-35417	Sequence 35417, A
36	37	46.2	15	6	US-10-490-949-2	Sequence 2, Appli
37	37	46.2	273	6	US-10-953-349-4464	Sequence 4464, Ap
38	37	46.2	305	7	US-11-293-697-4867	Sequence 4867, Ap
39	37	46.2	330	6	US-10-505-928-656	Sequence 656, App
40	37	46.2		6	US-10-953-349-4463	Sequence 4463, Ap
41	37	46.2		6	US-10-953-349-4462	Sequence 4462, Ap
42	37	46.2		6	US-10-511-937-2599	Sequence 2599, Ap
43	36	45.0		7	US-11-293-697-4833	Sequence 4833, Ap
44 45	36 35	45.0 43.8	666 246	7	US-11-293-697-3968 US-10-953-349-29161	Sequence 3968, Ap Sequence 29161, A
46	35	43.8	329	6 6	US-10-953-349-29161 US-10-953-349-29160	Sequence 29160, A
47	35	43.8	349	6	US-10-953-349-948	Sequence 948, App
48	35	43.8	352	6	US-10-953-349-21108	Sequence 21108, A
49	35	43.8	387	6	US-10-953-349-21107	Sequence 21107, A
50	35	43.8	396	6	US-10-953-349-21106	Sequence 21106, A
51	35	43.8	417	6	US-10-953-349-29159	Sequence 29159, A
52	35	43.8	419	6	US-10-953-349-1054	Sequence 1054, Ap
53	34	42.5		6	US-10-953-349-14698	Sequence 14698, A
54	34	42.5		7	US-11-122-986-185	Sequence 185, App
55	34	42.5		7	US-11-122-986-187	Sequence 187, App
56	33.5	41.9		6	US-10-953-349-7966	Sequence 7966, Ap
57	33.5	41.9	200	6	US-10-953-349-7965	Sequence 7965, Ap
58	33	41.2	138	6	US-10-953-349-20728	Sequence 20728, A
59	33	41.2	148	6	US-10-953-349-8299	Sequence 8299, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-12.rai.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 938-12.rai.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:12:07; Search time 12.7 Seconds

(without alignments)

103.383 Million cell updates/sec

Title:

US-10-001-938-12

Perfect score: 86

Sequence:

1 KKAYRRKALQWHPDK 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents AA:*

1: /EMC Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

> No. Score Match Length DB ID

용

Description

1	86	100.0	277	1	US-08-868-288A-7	Sequence 7, Appli
2	86	100.0	277	2	US-09-235-373-7	Sequence 7, Appli
3	86	100.0	277	2	US-09-388-993-7	Sequence 7, Appli
4	86	100.0	277	2	US-09-501-714-7	Sequence 7, Appli
5	86	100.0	327	2	US-09-949-016-11262	Sequence 11262, A
6	86	100.0	351	1	US-08-868-288A-6	Sequence 6, Appli
7	86	100.0	351	2	US-09-235-373-6	Sequence 6, Appli
8	86	100.0	351	2	US-09-388-993-6	Sequence 6, Appli
9	86	100.0	351	2	US-09-501-714-6	Sequence 6, Appli
10	72	83.7	330	1	US-08-868-288A-3	Sequence 3, Appli
11	72	83.7	330	2	US-09-235-373-3	Sequence 3, Appli
12	72	83.7	330	2	US-09-388-993-3	Sequence 3, Appli
13	72	83.7	330	2	US-09-501-714-3	Sequence 3, Appli
14	70	81.4	411	2	US-10-101-464A-982	Sequence 982, App
15	67	77.9	153	2	US-09-621-976-5129	Sequence 5129, Ap
16	66	76.7	340	1	US-08-974-546-5	Sequence 5, Appli
17	66	76.7	340	2	US-09-949-016-6691	Sequence 6691, Ap
18	66	76.7	363	2	US-09-949-016-8899	Sequence 8899, Ap
19	66	76.7	504	2	US-09-231-529-6	Sequence 6, Appli
20	66	76.7	504	2	US-08-977-816-6	Sequence 6, Appli
21	66	76.7	516	2	US-09-949-016-9654	Sequence 9654, Ap
22	65	75.6	334	3	US-10-429-223-3	Sequence 3, Appli
23	65	75.6	337	2	US-09-665-479A-8	Sequence 8, Appli
24	64	74.4	86	2	US-09-513-999C-6033	Sequence 6033, Ap
25	64	74.4	347	2	US-09-248-796A-19195	Sequence 19195, A
26	64	74.4	348	1	US-08-974-546-1	Sequence 1, Appli
27	64	74.4	397	2	US-09-248-796A-17628	Sequence 17628, A
28	64	74.4	595	2	US-10-104-047-2714	Sequence 2714, Ap
29	63	73.3	87	2	US-09-882-835-4	Sequence 4, Appli
30 31	63	73.3 73.3	102	2	US-09-513-999C-5137	Sequence 5137, Ap
31 32	63 63	73.3	118 127	2	US-09-248-796A-19798 US-09-370-838-199	Sequence 19798, A Sequence 199, App
33	63	73.3	127	2	US-09-854-133-199	Sequence 199, App
34	63	73.3	397	1	US-08-868-288A-5	Sequence 5, Appli
35	63	73.3	397	2	US-09-235-373-5	Sequence 5, Appli
36	63	73.3	397	2	US-09-388-993-5	Sequence 5, Appli
37	63	73.3	397	2	US-09-919-039-178	Sequence 178, App
38	63	73.3	397	2	US-09-538-092-1052	Sequence 1052, Ap
39	63	73.3	397	2	US-09-501-714-5	Sequence 5, Appli
40	63	73.3	397	3	US-10-429-223-2	Sequence 2, Appli
41	63	73.3	397	3	US-10-429-223-4	Sequence 4, Appli
42	62	72.1	51	1	US-08-346-849-12	Sequence 12, Appl
43	62	72.1	51	1	US-08-293-284A-12	Sequence 12, Appl
44	62	72.1	51	2	US-08-898-300-12	Sequence 12, Appl
45	62	72.1	51	2	US-08-824-513-12	Sequence 12, Appl
46	62	72.1	147	2	US-09-513-999C-6925	Sequence 6925, Ap
47	61	70.9	54	1	US-08-346-849-13	Sequence 13, Appl
48	61	70.9	54	1	US-08-293-284A-13	Sequence 13, Appl
49	61	70.9	54	2	US-08-898-300-13	Sequence 13, Appl
50	61	70.9	54	2	US-08-824-513-13	Sequence 13, Appl
51	61	70.9	381	2	US-09-252-991A-27174	Sequence 27174, A
52	60	69.8	49	1	US-08-346-849-11	Sequence 11, Appl
53	60	69.8	49	1	US-08-293-284A-11	Sequence 11, Appl
54	60	69.8	49	2	US-08-898-300-11	Sequence 11, Appl
55	60	69.8	49	2	US-08-824-513-11	Sequence 11, Appl
56	60	69.8	99	2	US-09-248-796A-19786	Sequence 19786, A
57	60	69.8	138	2	US-09-270-767-42296	Sequence 42296, A
58	60	69.8	358	1	US-08-868-288A-1	Sequence 1, Appli
59	60	69.8	358	2	US-09-235-373-1	Sequence 1, Appli
60	60	69.8	358	2	US-09-388-993-1	Sequence 1, Appli

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 12.rapbm.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

US-10-001-938-12 Title:

Perfect score: 86

1 KKAYRRKALQWHPDK 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2097797 segs, 463214858 residues Searched:

2097797 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published_Applications_AA_Main:* Database :

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
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                     153 4 US-10-424-599-257493
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3
                          4 US-10-424-599-257471
       73
             84.9
                     217
                                                        Sequence 257471,
 4
       73
             84.9
                     482 5 US-10-739-930-6446
                                                        Sequence 6446, Ap
 5
                      60 3 US-09-764-868-790
       72
             83.7
                                                        Sequence 790, App
                      60 3 US-09-764-891-3746
 6
       72
             83.7
                                                        Sequence 3746, Ap
7
       72
                             US-10-450-763-58941
             83.7
                     196
                                                        Sequence 58941, A
                         5
                                                        Sequence 22, Appl
8
       72
             83.7
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                     242
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                                                        Sequence 2674, Ap
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       72
             83.7
                     267
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                             US-09-764-868-1164
                                                        Sequence 1164, Ap
11
       72
            83.7
                     267
                         3 US-09-764-891-4089
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                     395
                         6 US-11-079-463-9803
                                                        Sequence 9803, Ap
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                     349 5 US-10-739-930-5915
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                      88 4 US-10-425-115-294867
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                                                        Sequence 24299, A
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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-12

Perfect score: 86

Sequence:

1 KKAYRRKALQWHPDK 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters:

58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result

1	No.	Score	Match	Length	DB	ID	Description
	1	86	100.0	15	6	US-10-490-949-21	Sequence 21, Appl
	2	73	84.9	465	6	US-10-953-349-8070	Sequence 8070, Ap
	3	73	84.9	473	6	US-10-953-349-8069	Sequence 8069, Ap
	4	73	84.9	482	6	US-10-953-349-8068	Sequence 8068, Ap
	5	71	82.6	349	6	US-10-953-349-948	Sequence 948, App
	6	70	81.4	335	6	US-10-953-349-2182	Sequence 2182, Ap
	7	70	81.4	336	6	US-10-953-349-33810	Sequence 33810, A
	8	70	81.4	343	6	US-10-953-349-2181	Sequence 2181, Ap
	9	70	81.4	430	6	US-10-953-349-33809	Sequence 33809, A
	10	66	76.7	15	6	US-10-490-949-22	Sequence 22, Appl
	11	66	76.7	504	6	US-10-511-937-2547	Sequence 2547, Ap
	12	63	73.3	15	6	US-10-490-949-23	Sequence 23, Appl
	13	63	73.3	397	7	US-11-293-697-3837	Sequence 3837, Ap
	14	59	68.6	119	6	US-10-953-349-28161	Sequence 28161, A
	15	59 50	68.6	147	6	US-10-953-349-28160	Sequence 28160, A
	16	59 50	68.6	155	6	US-10-953-349-28159	Sequence 28159, A
	17	59 59	68.6	190	6	US-10-953-349-28214	Sequence 28214, A
	18 19	59 59	68.6 68.6	191 426	6 7	US-10-953-349-28213 US-11-293-697-4751	Sequence 28213, A Sequence 4751, Ap
	20	58	67.4	95	6	US-10-953-349-31080	Sequence 31080, A
	21	58	67.4	156	6	US-10-953-349-5018	Sequence 5018, Ap
	22	56	65.1	420	6	US-10-953-349-13709	Sequence 13709, A
	23	55	64.0	15	6	US-10-490-949-3	Sequence 3, Appli
	24	55	64.0	340	6	US-10-953-349-24393	Sequence 24393, A
	25	55	64.0	427	6	US-10-953-349-24392	Sequence 24392, A
	26	55	64.0	445	6	US-10-953-349-24391	Sequence 24391, A
	27	55	64.0	530	6	US-10-953-349-20585	Sequence 20585, A
	28	54	62.8	199	6	US-10-953-349-9116	Sequence 9116, Ap
	29	54	62.8	248	6	US-10-953-349-9115	Sequence 9115, Ap
	30	53	61.6	305	6	US-10-953-349-23847	Sequence 23847, A
	31	53	61.6	317	6	US-10-953-349-11729	Sequence 11729, A
	32	53	61.6	417	6	US-10-953-349-16377	Sequence 16377, A
	33	53	61.6	419	6	US-10-953-349-1054	Sequence 1054, Ap
	34	52	60.5	273	6	US-10-953-349-4464	Sequence 4464, Ap
	35	52	60.5	349	6	US-10-953-349-4463	Sequence 4463, Ap
	36	52	60.5	367	6	US-10-953-349-4462	Sequence 4462, Ap
	37	51	59.3	391	6 6	US-10-953-349-7627 US-10-953-349-22808	Sequence 7627, Ap
	38 39	49 49	57.0	250 389	7	US-11-122-986-185	Sequence 22808, A Sequence 185, App
	40	49	57.0 57.0	389		US-11-122-986-187	Sequence 187, App
	41	48	55.8	379		US-10-953-349-11645	Sequence 11645, A
	42	47	54.7	422	6	US-10-953-349-17849	Sequence 17849, A
	43	47	54.7	453	6	US-10-953-349-17848	Sequence 17848, A
	44	47	54.7	467	6	US-10-953-349-17847	Sequence 17847, A
	45	47	54.7	583	6	US-10-953-349-35418	Sequence 35418, A
	46	47	54.7	630	6	US-10-953-349-35417	Sequence 35417, A
	47	46	53.5	313	6	US-10-953-349-23774	Sequence 23774, A
	48	46	53.5	334	6	US-10-953-349-23773	Sequence 23773, A
	49	46	53.5	380	6	US-10-953-349-7175	Sequence 7175, Ap
	50	46	53.5	391	6	US-10-953-349-7174	Sequence 7174, Ap
	51	46	53.5	442	6	US-10-953-349-7173	Sequence 7173, Ap
	52	46	53.5	605	6	US-10-953-349-2076	Sequence 2076, Ap
	53	46	53.5	619		US-10-953-349-2075	Sequence 2075, Ap
	54	46	53.5	630	6	US-10-953-349-2074	Sequence 2074, Ap
	55	45	52.3	138	6	US-10-953-349-39107	Sequence 39107, A
	56	45	52.3	174	6	US-10-953-349-39106	Sequence 39106, A
	57 50	45 45	52.3	338	6	US-10-953-349-20361	Sequence 20361, A
	58 50	45 45	52.3		6 6	US-10-953-349-20360	Sequence 20360, A
	59	45	52.3	488	О	US-10-953-349-20359	Sequence 20359, A

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OM protein - protein search, using sw model

June 2, 2006, 19:12:07; Search time 12.7 Seconds Run on:

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-13

Perfect score: 82

Sequence: 1 KRAYRROALRYHPDK 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.			Length	DB	ID	Description	
1 2	82 82	100.0	340 340		US-08-974-546-5 US-09-949-016-6691	Sequence 5, Appli Sequence 6691, Ap	

3	82	100.0	363	2	US-09-949-016-8899	Sequence 889	_
4	69	84.1	334	3	US-10-429-223-3	Sequence 3,	
5	69	84.1	337	2	US-09-665-479A-8	Sequence 8,	
6	68	82.9	348	1	US-08-974-546-1	Sequence 1,	
7	67	81.7	54	1	US-08-346-849-13	Sequence 13,	
8	67	81.7	54	1	US-08-293-284A-13	Sequence 13,	Appl
9	67	81.7	54	2	US-08-898-300-13	Sequence 13,	Appl
10	67	81.7	54	2	US-08-824-513-13	Sequence 13,	Appl
11	67	81.7	347	2	US-09-248-796A-19195	Sequence 191	.95, A
12	67	81.7	397	2	US-09-248-796A-17628	Sequence 176	528, A
13	66	80.5	87	2	US-09-882-835-4	Sequence 4,	Appli
14	66	80.5	102	2	US-09-513-999C-5137	Sequence 513	37, Ap
15	66	80.5	127	2	US-09-370-838-199	Sequence 199	App
16	66	80.5	127	2	US-09-854-133-199	Sequence 199	App
17	66	80.5	277	1	US-08-868-288A-7	Sequence 7,	Appli
18	66	80.5	277	2	US-09-235-373-7	Sequence 7,	Appli
19	66	80.5	277	2	US-09-388-993-7	Sequence 7,	
20	66	80.5	277	2	US-09-501-714-7	Sequence 7,	
21	66	80.5	327	2	US-09-949-016-11262	Sequence 112	
22	66	80.5	351	1	US-08-868-288A-6	Sequence 6,	
23	66	80.5	351	2	US-09-235-373-6	Sequence 6,	
24	66	80.5	351	2	US-09-388-993-6	Sequence 6,	
25	66	80.5	351	2	US-09-501-714-6	Sequence 6,	
26	66	80.5	397	1	US-08-868-288A-5	Sequence 5,	
27	66	80.5	397	2	US-09-235-373-5	Sequence 5,	
28	66	80.5	397	2	US-09-388-993-5	Sequence 5,	
29	66	80.5	397	2	US-09-919-039-178	Sequence 178	
30	66	80.5	397	2	US-09-538-092-1052	Sequence 105	
31	66	80.5	397	2	US-09-501-714-5	Sequence 5,	_
32	66	80.5	397	3	US-10-429-223-2	Sequence 2,	
33	66	80.5	397	3	US-10-429-223-4	Sequence 4,	
34	66	80.5	734	2	US-09-248-796A-16776	Sequence 167	
35	65	79.3	51	1	US-08-346-849-12	Sequence 12,	
36	65	79.3	51	1	US-08-293-284A-12	Sequence 12,	
37	65	79.3	51	2	US-08-898-300-12	Sequence 12,	
38	65	79.3	51	2	US-08-824-513-12	Sequence 12,	
39	64	78.0	380	2	US-09-543-681A-5912	Sequence 591	
40	64	78.0	381	2	US-09-252-991A-27174	Sequence 271	
41	63	76.8	49	1	US-08-346-849-11	Sequence 11,	
42	63	76.8	49	1	US-08-293-284A-11	Sequence 11,	
43	63	76.8	49	2	US-08-898-300-11	Sequence 11,	
44	63	76.8	49	2	US-08-824-513-11	Sequence 11,	
45	63	76.8	99	2	US-09-248-796A-19786	Sequence 19	
46	63	76.8	147	2	US-09-270-767-33311	Sequence 333 Sequence 485	
47	63	76.8	147	2	US-09-270-767-48528	-	-
48	63	76.8	392	2	US-09-198-452A-48	Sequence 48,	
49	63	76.8	406	2	US-09-438-185A-34	Sequence 34,	
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51	62	75.6	52	1	US-08-293-284A-10	Sequence 10	
52	62	75.6	52	2	US-08-898-300-10	Sequence 10	
53	62	75.6	52	2	US-08-824-513-10	Sequence 10	
54	62	75.6	147	2	US-09-513-999C-6925	Sequence 692	
55	62	75.6	286	2	US-09-248-796A-16992	Sequence 169	
56	61	74.4	330	1	US-08-868-288A-3	Sequence 3,	
57	61	74.4	330	2	US-09-235-373-3	Sequence 3,	
58	61	74.4	330	2	US-09-388-993-3	Sequence 3,	
59	61	74.4	330	2	US-09-501-714-3	Sequence 3,	
60	61	74.4	375	2	US-09-328-352-4984	Sequence 498	
61	61	74.4	380	2	US-09-489-039A-9011	Sequence 90:	-
62	60	73.2	308	2	US-09-248-796A-19781	Sequence 19	
63	60	73.2	411	2	US-10-101-464A-982	Sequence 982	z, App

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-13.rapbm.

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OM protein - protein search, using sw model

June 2, 2006, 19:45:16; Search time 63.4 Seconds Run on:

> (without alignments) 109.593 Million cell updates/sec

Title: US-10-001-938-13

Perfect score: 82

Sequence: 1 KRAYRRQALRYHPDK 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

용 Result Query No. Score Match Length DB ID Description 82 100.0 15 4 US-10-001-938-13 Sequence 13, Appl

2	0.2	100.0	70	6	US-11-047-063-1	Comiones	1 Appli
2	82						1, Appli
3	82	100.0	340	4	US-10-116-275-134		134, App
4	82	100.0	340	4	US-10-116-275-135	-	135, App
5	82	100.0	340	5	US-10-871-388-5	_	5, Appli
6	82	100.0	340	5	US-10-792-571-16		16, Appl
7	82	100.0	340	6	US-11-047-063-2		2, Appli
8	82	100.0	377	5	US-10-450-763-48884	Sequence	48884, A
9	73	89.0	405	5	US-10-450-763-48886	Sequence	48886, A
10	70	85.4	128	6	US-11-097-143-15807	Sequence	15807, A
11	69	84.1	193	3	US-09-925-301-983	Sequence	983, App
12	69	84.1	224	4	US-10-424-599-280547	Sequence	
13	69	84.1	334	4	US-10-429-223-3		3, Appli
14	69	84.1	335	6	US-11-097-143-10161	-	10161, A
15	69	84.1	337	4	US-10-788-792-162	_	162, App
16	69	84.1	344	4	US-10-424-599-280548	Sequence	
17	69	84.1	346	5	US-10-739-930-5798		5798, Ap
18	68	82.9	138	3	US-09-764-868-786		
							786, App
19	68	82.9	342	6	US-11-097-143-3567		3567, Ap
20	68	82.9	348	5	US-10-871-388-1	=	1, Appli
21	67	81.7	54	4	US-10-390-472-13	-	13, Appl
22	67	81.7	158	4	US-10-425-114-48912	=	48912, A
23	67	81.7	170	4	US-10-767-701-59629	Sequence	59629, A
24	67	81.7	268	4	US-10-425-115-232395	Sequence	232395,
25	67	81.7	326	4	US-10-425-115-300448	Sequence	300448,
26	67	81.7	329	4	US-10-437-963-123301	Sequence	123301,
27	66	80.5	15	4	US-10-001-938-12	Sequence	12, Appl
28	66	80.5	15	4	US-10-001-938-14		14, Appl
29	66	80.5	66	6	US-11-039-722-7		7, Appli
30	66	80.5	87	4	US-10-145-586-48		48, Appl
31	66	80.5	127	3	US-09-738-973-199		199, App
32	66	80.5	127	3	US-09-854-133-199	_	199, App
33	66	80.5	127	4	US-10-144-649A-199	_	
34			150	4		_	199, App
	66	80.5		-	US-10-425-115-206200	Sequence	
35	66	80.5	154	4	US-10-424-599-217994	Sequence	
36	66	80.5	329	4	US-10-425-115-319609	Sequence	
37	66	80.5	334	4	US-10-161-051-134	_	134, App
38	66	80.5	334	6	US-11-097-143-22242		22242, A
39	66	80.5	347	4	US-10-437-963-150219	Sequence	
40	66	80.5	350	5	US-10-739-930-9807		9807, Ap
41	66	80.5	379	4	US-10-369-493-22783		22783, A
42	66	80.5	395	6	US-11-079-463-9803	Sequence	9803, Ap
43	66	80.5	397	3	US-09-919-039-178	Sequence	178, App
44	66	80.5	397	4	US-10-108-260A-3837	Sequence	3837, Ap
45	66	80.5	397	4	US-10-429-223-2	Sequence	2, Appli
46	66	80.5	397	4	US-10-429-223-4	Sequence	4, Appli
47	66	80.5	397	5	US-10-473-127-1138		1138, Ap
48	66	80.5	397	5	US-10-473-127-1139		1139, Ap
49	66	80.5	397	5	US-10-473-127-1140		1140, Ap
50	66	80.5	397	5	US-10-473-127-1143	_	1143, Ap
51	66	80.5	397	5	US-10-473-127-1144		1144, Ap
52	66	80.5	397	5	US-10-473-127-1145		1144, Ap
53	66			5		_	_
		80.5	397		US-10-756-149-4727		4727, Ap
54	66	80.5	397	5	US-10-631-467-559		559, App
55	66	80.5	397	5	US-10-631-467-1386		1386, Ap
56	66	80.5	397	5	US-10-878-556A-155	_	155, App
57	66	80.5	403	6	US-11-097-143-24405		24405, A
58	66	80.5	403	6	US-11-097-143-41904		41904, A
59	66	80.5	408	5	US-10-450-763-40099		40099, A
60	65	79.3	51	4	US-10-390-472-12		12, Appl
61	65	79.3	119	4	US-10-389-566-776		776, App
62	65	79.3	171	4	US-10-425-115-211529	Sequence	211529,

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-13.rapbn.

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Comments / Suggestions

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-13.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-13

Perfect score: 82

Sequence:

1 KRAYRRQALRYHPDK 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description
1	82	100.0	15	6	US-10-490-949-22	Sequence 22, Appl
2	66	80.5	15	6	US-10-490-949-21	Sequence 21, Appl
3	66	80.5	15	6	US-10-490-949-23	Sequence 23, Appl
4	66	80.5	397	7	US-11-293-697-3837	Sequence 3837, Ap
5	62	75.6	336	6	US-10-953-349-33810	Sequence 33810, A
6	62	75.6	430	6	US-10-953-349-33809	Sequence 33809, A
7	61	74.4	349	6	US-10-953-349-948	Sequence 948, App
8	59	72.0	199	6	US-10-953-349-9116	Sequence 9116, Ap
9	59	72.0	248	6	US-10-953-349-9115	Sequence 9115, Ap
10	59	72.0	335	6	US-10-953-349-2182	Sequence 2182, Ap
11	59	72.0	343	6	US-10-953-349-2181	Sequence 2181, Ap
12	58	70.7	15	6	US-10-490-949-3	Sequence 3, Appli
13	58 57	70.7	530	6	US-10-953-349-20585	Sequence 20585, A
14 15	57 57	69.5 69.5	426 465	7 6	US-11-293-697-4751	Sequence 4751, Ap
16	5 <i>7</i>	69.5	473	6	US-10-953-349-8070 US-10-953-349-8069	Sequence 8070, Ap
17	5 <i>7</i>	69.5	482	6	US-10-953-349-8069 US-10-953-349-8068	Sequence 8069, Ap Sequence 8068, Ap
18	56	68.3	305	6	US-10-953-349-23847	Sequence 23847, A
19	56	68.3	420	6	US-10-953-349-13709	Sequence 13709, A
20	54	65.9	119	6	US-10-953-349-28161	Sequence 28161, A
21	54	65.9	147	6	US-10-953-349-28160	Sequence 28160, A
22	54	65.9	155	6	US-10-953-349-28159	Sequence 28159, A
23	54	65.9	190	6	US-10-953-349-28214	Sequence 28214, A
24	54	65.9	191	6	US-10-953-349-28213	Sequence 28213, A
25	53	64.6	417	6	US-10-953-349-16377	Sequence 16377, A
26	53	64.6	419	6	US-10-953-349-1054	Sequence 1054, Ap
27	52	63.4	273	6	US-10-953-349-4464	Sequence 4464, Ap
28	52	63.4	349	6	US-10-953-349-4463	Sequence 4463, Ap
29	52	63.4	367	6	US-10-953-349-4462	Sequence 4462, Ap
30	52	63.4	389	7	US-11-122-986-185	Sequence 185, App
31	52	63.4	389	7	US-11-122-986-187	Sequence 187, App
32	51	62.2	189	7	US-11-293-697-4556	Sequence 4556, Ap
33	50	61.0	95	6	US-10-953-349-31080	Sequence 31080, A
34	50	61.0	156	6	US-10-953-349-5018	Sequence 5018, Ap
35	50	61.0	333	6	US-10-953-349-2863	Sequence 2863, Ap
36	50	61.0	333	6	US-10-953-349-11247	Sequence 11247, A
37 38	50 50	61.0	340 380	6 6	US-10-953-349-24393	Sequence 24393, A
	50 50	61.0		_	US-10-953-349-7175	Sequence 7175, Ap
39 40	50 50	61.0 61.0	391 427	6 6	US-10-953-349-7174 US-10-953-349-24392	Sequence 7174, Ap Sequence 24392, A
41	50	61.0	442	6	US-10-953-349-7173	Sequence 7173, Ap
42	50	61.0	445	6	US-10-953-349-24391	Sequence 24391, A
43	50	61.0	504	6	US-10-511-937-2547	Sequence 2547, Ap
44	50	61.0	583	6	US-10-953-349-35418	Sequence 35418, A
45	50	61.0	630	6	US-10-953-349-35417	Sequence 35417, A
46	49	59.8	110	6	US-10-953-349-54	Sequence 54, Appl
47	49	59.8	124	6	US-10-953-349-53	Sequence 53, Appl
48	49	59.8	162	6	US-10-953-349-52	Sequence 52, Appl
49	49	59.8	605	6	US-10-953-349-2076	Sequence 2076, Ap
50	49	59.8	619	6	US-10-953-349-2075	Sequence 2075, Ap
51	49	59.8	630	6	US-10-953-349-2074	Sequence 2074, Ap
52	48	58.5	338	6	US-10-953-349-20361	Sequence 20361, A
53	48	58.5	385	6	US-10-953-349-20360	Sequence 20360, A
54	48	58.5	488	6	US-10-953-349-20359	Sequence 20359, A
55	47	57.3	250	6	US-10-953-349-22808	Sequence 22808, A
56 57	46	56.1	313	6	US-10-953-349-23774	Sequence 23774, A
57 50	46	56.1	334	6	US-10-953-349-23773	Sequence 23773, A
58 59	45 45	54.9 54.9	317 422	6 6	US-10-953-349-11729 US-10-953-349-17849	Sequence 11729, A Sequence 17849, A
33	40	J4.3	422	U	OD-10-903-349-17049	sequence 1/043, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-14.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:08:52; Search time 11.4238 Seconds

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-14

Perfect score: 81

Sequence: 1 KKAYRKLALKYHPDK 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Score Match L			ID	Description		
1	81	100.0		_	US-09-882-835-4	Sequence 4, Appli		
2	81	100.0	102	2	US-09-513-999C-5137	Sequence 5137, Ap		

3	81	100.0	127	2	US-09-370-838-199	Sequence	199, App
4	81	100.0	127	2	US-09-854-133-199	Sequence	199, App
5	81	100.0	397	1	US-08-868-288A-5	Sequence	5, Appli
6	81	100.0	397	2	US-09-235-373-5	Sequence	5, Appli
7	81	100.0	397	2	US-09-388-993-5	Sequence	5, Appli
8	81	100.0	397	2	US-09-919-039-178	Sequence	
9	81	100.0	397	2	US-09-538-092-1052	Sequence	
10	81	100.0	397	2	US-09-501-714-5	Sequence	
11	81	100.0	397	3	US-10-429-223-2	Sequence	
			397	3	US-10-429-223-4	_	
12	81	100.0				Sequence	
13	79	97.5	348	1	US-08-974-546-1	Sequence	
14	78	96.3	392	2	US-09-198-452A-48	Sequence	
15	78	96.3	406	2	US-09-438-185A-34	Sequence	
16	77	95.1	52	1	US-08-346-849-10	Sequence	
17	77	95.1	52	1	US-08-293-284A-10	Sequence	
18	77	95.1	52	2	US-08-898-300-10	Sequence	10, Appl
19	77	95.1	52	2	US-08-824-513-10	Sequence	10, Appl
20	77	95.1	147	2	US-09-513-999C-6925	Sequence	6925, Ap
21	76	93.8	51	1	US-08-346-849-12	Sequence	12, Appl
22	76	93.8	51	1	US-08-293-284A-12	Sequence	
23	76	93.8	51	2	US-08-898-300-12	Sequence	
24	76	93.8	51	2	US-08-824-513-12	Sequence	
			330		US-08-868-288A-3	Sequence	
25	76	93.8		1			
26	76	93.8	330	2	US-09-235-373-3	Sequence	
27	76	93.8	330	2	US-09-388-993-3	Sequence	
28	76	93.8	330	2	US-09-501-714-3	Sequence	
29	76	93.8	347	2	US-09-248 - 796A-19195	Sequence	
30	76	93.8	375	2	US-09-328-352-4984	Sequence	4984, Ap
31	76	93.8	397	2	US-09-248 - 796A-17628	Sequence	17628, A
32	73	90.1	381	2	US-09-252-991A-27174	Sequence	27174, A
33	72	88.9	49	1	US-08-346-849-11	Sequence	11, Appl
34	72	88.9	49	1	US-08-293-284A-11	Sequence	11, Appl
35	72	88.9	49	2	US-08-898-300-11	Sequence	
36	72	88.9	49	2	US-08-824-513-11	Sequence	
37	71	87.7	75	2	US-09-513-999C-6016	Sequence	
38	71	87.7	334	3	US-10-429-223-3	Sequence	
39	71	87.7	337	2	US-09-665-479A-8	Sequence	
40	70	86.4	96	2	US-09-621-976-4045	Sequence	
				2	US-09-248-796A-16959	-	
41	70	86.4	199			Sequence	
42	70	86.4	223	2	US-09-658-644-4	Sequence	
43	70	86.4	223	2	US-09-949-016-6832	_	6832, Ap
44	70	86.4	267	2	US-09-949-016-11497		11497, A
45	70	86.4	320	2	US-09-328-352-7937	_	7937, Ap
46	70	86.4	380	2	US-09-489-039A-9011		9011, Ap
47	70	86.4	382	2	US-09-603-208A-40	Sequence	40, Appl
48	70	86.4	391	2	US-09-902-540-11110	Sequence	11110, A
49	70	86.4	407	2	US-09-540-236-2899	Sequence	2899, Ap
50	69	85.2	734	. 2	US-09-248-796A-16776	Sequence	16776, A
51	68	84.0	153	2	US-09-621-976-5129		5129, Ap
52	67	82.7	52	1	US-08-346-849-8		8, Appli
53	67	82.7	52	1	US-08-293-284A-8	Sequence	
54	67	82.7	52	2	US-08-898-300-8	-	8, Appli
			52 52	2			8, Appli
55 56	67	82.7			US-08-824-513-8	_	
56	67	82.7	54	1	US-08-346-849-13		13, Appl
57	67	82.7	54	1	US-08-293-284A-13		13, Appl
58	67	82.7	54	2	US-08-898-300-13		13, Appl
59	67	82.7	54	2	US-08-824-513-13		13, Appl
60	67	82.7	95	2	US-09-248-796A-19797		19797, A
61	67	82.7	131	2	US-09-553-498-4		4, Appli
62	67	82.7	131	2	US-09-618-869-4		4, Appli
63	67	82.7	206	2	US-09-830-230A-294	Sequence	294, App

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 14.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 14.rapbm.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:29:53; Search time 75.9934 Seconds

(without alignments)

91.432 Million cell updates/sec

US-10-001-938-14 Title:

Perfect score: 81

1 KKAYRKLALKYHPDK 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA Main:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

> 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length DB ID			Description		
1	81	100.0	15	 4	US-10-001-938-14	Sequence 14, Appl		

				_			_	
2	81	100.0	66	6	US-11-039-722-7			, Appli
3	81	100.0	87	4	US-10-145-586-48	Sequer	nce 48	8, Appl
4	81	100.0	127	3	US-09-738-973-199	Seguer	nce 1	99, App
5	81	100.0	127	3	US-09-854-133-199			99, App
6			127	4	US-10-144-649A-199	_		
	81	100.0				_		99, App
7	81	100.0	150	4	US-10-425-115-206200			06200,
8	81	100.0	154	4	US-10-424-599-217994	Sequer	nce 2	17994,
9	81	100.0	334	4	US-10-161-051-134	Sequer	nce 13	34, App
10	81	100.0	334	6	US-11-097-143-22242	_		2242, A
11	81	100.0	379	4	US-10-369-493-22783	_		2783, A
						_		
12	81	100.0	397	3	US-09-919-039-178	-		78, App
13	81	100.0	397	4	US-10-108-260A-3837			837, Ap
14	81	100.0	397	4	US-10-429-223-2	Sequer	nce 2	, Appli
15	81	100.0	397	4	US-10-429-223-4	Seguer	nce 4	, Appli
16	81	100.0	397	5	US-10-473-127-1138			138, Ap
17	81	100.0	397	5	US-10-473-127-1139			139, Ap
				5		_		_
18	81	100.0	397		US-10-473-127-1140			140, Ap
19	81	100.0	397	5	US-10-473-127-1143			143, Ap
20	81	100.0	397	5	US-10-473-127-1144	Sequer	nce 1	144, Ap
21	81	100.0	397	5	US-10-473-127-1145	Sequer	nce 1	145, Ap
22	81	100.0	397	5	US-10-756-149-4727			727, Ap
23	81	100.0	397	5	US-10-631-467-559	-		59, App
						_		
24	81	100.0	397	5	US-10-631-467-1386	_		386, Ap
25	81	100.0	397	5	US-10-878-556A-155	-		55, App
26	81	100.0	403	6	US-11-097-143-24405	Sequer	nce 2	4405, A
27	81	100.0	403	6	US-11-097-143-41904	Sequer	nce 4	1904, A
28	81	100.0	408	5	US-10-450-763-40099	Sequer	nce 4	0099, A
29	79	97.5	138	3	US-09-764-868-786	_		86, App
30	79	97.5	348	5	US-10-871-388-1	_		, Appli
31	79	97.5	485	4	US-10-369-493-12487	_		2487, A
32	78	96.3	183	3	US-09-764-868-787			87, App
33	78	96.3	198	5	US-10-494-921-51	Sequei	nce 5	1, Appl
34	78	96.3	224	4	US-10-424-599-280547	Sequer	nce 2	80547,
35	78	96.3	335	6	US-11-097-143-10161	Seque	nce 1	0161, A
36	78	96.3	344	4	US-10-424-599-280548	_		80548,
37	78	96.3	346	5	US-10-739-930-5798			798, Ap
						_		_
38	78	96.3	392	4	US-10-289-762-48	_		8, Appl
39	77	95.1	52	4	US-10-390-472-10			0, Appl
40	77	95.1	132	3	US-09-764-868-1163			163, Ap
41	77	95.1	220	5	US-10-494-921-52	Sequei	nce 5.	2, Appl
42	77	95.1	223	6	US-11-097-143-41196	Sequei	nce 4	1196, A
43	77	95.1	249	6	US-11-097-143-24078			4078, A
44	77	95.1	276	4	US-10-220-120-320	-		20, App
			297	_	US-09-764-868-1162	_		162, Ap
45	77	95.1		3		-		_
46	77	95.1	373	3	US-09-764-868-789	_		89, App
47	77	95.1	379	5	US-10-489-695-9			, Appli
48	77	95.1	397	3	US-09-989-890-262	Sequei	nce 2	62, App
49	76	93.8	51	4	US-10-390-472-12	Sequei	nce 1	2, Appl
50	76	93.8	60	3	US-09-764-868-790	-		90, App
51	76	93.8	60	3	US-09-764-891-3746	-		746, Ap
								9994, A
52	76	93.8	112	4	US-10-767-701-39994			
53	76	93.8	143	4	US-10-424-599-230584			30584,
54	76	93.8	158	4	US-10-425-114-48912			8912, A
55	76	93.8	196	5	US-10-450-763-58941	Seque	nce 5	8941, A
56	76	93.8	242	4	US-10-264-049-2674	Seque	nce 2	674, Ap
57	76	93.8	255	4	US-10-437-963-123368			23368,
58	76	93.8	276	4	US-10-282-122A-47226			7226, A
59	76	93.8	326	4	US-10-425-115-300448			00448,
60	76	93.8	369	4	US-10-369-493-19646	_		9646, A
61	76	93.8	407	4	US-10-425-115-303598	-		03598,
62	76	93.8	413	4	US-10-425-114-56774	Seque	nce 5	6774, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-14.rapbn.

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SCORE System Overview

SCORE FAO Comments / Suggestions

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-14.rapbn.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title:

US-10-001-938-14

Perfect score: 81

Sequence: 1

1 KKAYRKLALKYHPDK 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

_

Result Query

No.	Score	Match	Length	DB	ID	Description
1	81	100.0	15	6	US-10-490-949-23	Sequence 23, Appl
2	81	100.0	397	7	US-11-293-697-3837	Sequence 3837, Ap
3	74	91.4	335	6	US-10-953-349-2182	Sequence 2182, Ap
4	74	91.4	343	6	US-10-953-349-2181	Sequence 2181, Ap
5	72	88.9	426	7	US-11-293-697-4751	Sequence 4751, Ap
6	71	87.7	305	6	US-10-953-349-23847	Sequence 23847, A
7	71	87.7	336	6	US-10-953-349-33810	Sequence 33810, A
8	71	87.7	430	6	US-10-953-349-33809	Sequence 33809, A
9	69	85.2	465	6	US-10-953-349-8070	Sequence 8070, Ap
10	69	85.2	473	6	US-10-953-349-8069	Sequence 8069, Ap
11	69	85.2	482	6	US-10-953-349-8068	Sequence 8068, Ap
12	67	82.7	15	6	US-10-490-949-3	Sequence 3, Appli
13	67	82.7	273	6	US-10-953-349-4464	Sequence 4464, Ap
14	67	82.7	349	6	US-10-953-349-4463	Sequence 4463, Ap
15	67	82.7	367	6	US-10-953-349-4462	Sequence 4462, Ap
16	67	82.7	389	7	US-11-122-986-185	Sequence 185, App
17	67	82.7	389	7	US-11-122-986-187	Sequence 187, App
18	66	81.5	15	6	US-10-490-949-22	Sequence 22, Appl
19	66	81.5	199	6	US-10-953-349-9116	Sequence 9116, Ap
20	66	81.5	248	6	US-10-953-349-9115	Sequence 9115, Ap
21	66	81.5	349	6	US-10-953-349-948	Sequence 948, App
22	65	80.2	420	6	US-10-953-349-13709	Sequence 13709, A
23	65	80.2	583	6	US-10-953-349-35418	Sequence 35418, A
24	65	80.2	630	6	US-10-953-349-35417	Sequence 35417, A
25	63	77.8	15	6	US-10-490-949-21	Sequence 21, Appl
26	62	76.5	95	6	US-10-953-349-31080	Sequence 31080, A
27	62	76.5	156	6	US-10-953-349-5018	Sequence 5018, Ap
28	62	76.5	417	6	US-10-953-349-16377	Sequence 16377, A
29	62	76.5	419	6	US-10-953-349-1054	Sequence 1054, Ap
30	62	76.5	504	6	US-10-511-937-2547	Sequence 2547, Ap
31	61	75.3	313	6	US-10-953-349-23774	Sequence 23774, A
32	61	75.3	334	6	US-10-953-349-23773	Sequence 23773, A
33	60	74.1	380	6	US-10-953-349-7175	Sequence 7175, Ap
34	60	74.1	391	6	US-10-953-349-7174	Sequence 7174, Ap
35	60	74.1	442	6	US-10-953-349-7173	Sequence 7173, Ap
36	59	72.8	250	6	US-10-953-349-22808	Sequence 22808, A
37	59	72.8	530	6	US-10-953-349-20585	Sequence 20585, A
38	58	71.6	110	6	US-10-953-349-54	Sequence 54, Appl
39	58	71.6	124	6	US-10-953-349-53	Sequence 53, Appl
40	58	71.6	162	6	US-10-953-349-52	Sequence 52, Appl
41	57	70.4		7	US-11-293-697-4556	Sequence 4556, Ap
42	56	69.1	333	6	US-10-953-349-2863	Sequence 2863, Ap
43	56	69.1	333	6	US-10-953-349-11247	Sequence 11247, A
44	54	66.7	190	6	US-10-953-349-28214	Sequence 28214, A
45	54	66.7	191	6	US-10-953-349-28213	Sequence 28213, A
46	53	65.4	340	6	US-10-953-349-24393	Sequence 24393, A
47	53	65.4	427	6	US-10-953-349-24392	Sequence 24392, A
48	53	65.4	445	6	US-10-953-349-24391	Sequence 24391, A
49	52	64.2	157	6	US-10-953-349-38105	Sequence 38105, A
50 51	52	64.2	192	6	US-10-953-349-38104	Sequence 38104, A
51 52	51	63.0		6	US-10-953-349-17849	Sequence 17849, A
52	51	63.0		6	US-10-953-349-17848	Sequence 17848, A
53	51	63.0		6	US-10-953-349-17847	Sequence 17847, A
54 55	49	60.5		6	US-10-953-349-2076	Sequence 2076, Ap
55 56	49	60.5		6	US-10-953-349-2075	Sequence 2075, Ap
56	49	60.5	630	6	US-10-953-349-2074	Sequence 2074, Ap
57 50	48	59.3		6	US-10-953-349-28161	Sequence 28161, A
58 59	48	59.3		6	US-10-953-349-39107	Sequence 39107, A
39	48	59.3	147	6	US-10-953-349-28160	Sequence 28160, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-15

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 15.rai.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:08:52; Search time 11.4238 Seconds

(without alignments)

114.932 Million cell updates/sec

Title:

US-10-001-938-15

Perfect score: 73

Sequence: 1 FRSVSTSTTFVQGRR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters:

650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents AA:*

1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query No. Score Match Length DB ID Description 73 100.0 277 1 US-08-868-288A-7 73 100.0 277 2 US-09-235-373-7 1 Sequence 7, Appli Sequence 7, Appli 2

_	7.0	100 0	077	_	*** 00 300 003 7	o 7	
3	73	100.0	277	2	US-09-388-993-7	Sequence 7, Appli	
4	73	100.0	277	2	US-09-501-714-7	Sequence 7, Appli	
5	73	100.0	327	2	US-09-949-016-11262	Sequence 11262, F	
6	73	100.0	351	1	US-08-868-288A-6	Sequence 6, Appli	
7	73	100.0	351	2	US-09-235-373-6	Sequence 6, Appli	
8	73	100.0	351	2	US-09-388-993-6	Sequence 6, Appli	L
9	73	100.0	351	2	US-09-501-714-6	Sequence 6, Appli	L
10	49	67.1	330	1	US-08-868-288A-3	Sequence 3, Appli	L
11	49	67.1	330	2	US-09-235-373-3	Sequence 3, Appli	
12	49	67.1	330	2	US-09-388-993-3	Sequence 3, Appli	
13	49	67.1	330	2	US-09-501-714-3	Sequence 3, Appli	
14	40	54.8	83	2	US-09-107-433-4269	Sequence 4269, Ap	
15	40	54.8	108	2	US-09-107-433-5049	Sequence 5049, Ap	
16	38	52.1	269	2	US-09-252-991A-24237	Sequence 24237, A	
17			339	2	US-10-104-047-2843	<u>-</u>	
	38	52.1				Sequence 2843, Ap	
18	38	52.1	540	2	US-10-104-047-3747	Sequence 3747, Ap	
19	37	50.7	165	2	US-09-270-767-37910	Sequence 37910, A	
20	37	50.7	165	2	US-09-270-767-53127	Sequence 53127, F	
21	37	50.7	464	2	US-09-693-746-14	Sequence 14, Appl	
22	37	50.7	1271	1	US-08-095-734-2	Sequence 2, Appli	L
23	37	50.7	1271	1	US-08-444-623-2	Sequence 2, Appli	L
24	37	50.7	1271	2	US-08-471-869-2	Sequence 2, Appli	Ĺ
25	37	50.7	1271	2	US-09-342-563-2	Sequence 2, Appli	
26	37	50.7	1271	5	PCT-US94-08267-2	Sequence 2, Appli	
27	36	49.3	102	2	US-09-471-276-1004	Sequence 1004, Ap	
28	36	49.3	103	2	US-09-673-395A-348	Sequence 348, App	
29	36	49.3	108	2	US-09-107-433-5048	Sequence 5048, Ap	
30	36	49.3	108	2	US-09-107-433-5050	Sequence 5050, Ap	
31	36	49.3	476	2	US-09-902-540-14917	Sequence 14917, A	
32	36	49.3	788	1	US-08-194-338-12	-	
						Sequence 12, Appl	
33	36	49.3	859	1	US-08-053-614-2	Sequence 2, Appli	
34	36	49.3	859	1	US-08-316-397B-2	Sequence 2, Appli	
35	36	49.3	859	1	US-09-034-306-2	Sequence 2, Appli	
36	36	49.3	859	2	US-09-259-437-2	Sequence 2, Appli	
37	36	49.3	859	5	PCT-US93-09782-2	Sequence 2, Appli	
38	36	49.3	1041	2	US-09-999-833A-498	Sequence 498, App	
39	36	49.3	1041	2	US-09-954-987B-184	Sequence 184, App)
40	36	49.3	1041	2	US-09-954-987B-186	Sequence 186, App	>
41	36	49.3	1041	2	US-10-020-445A-498	Sequence 498, App	>
42	36	49.3	1041	2	US-09-978-189-498	Sequence 498, App	Ç
43	36	49.3	1041	2	US-10-017-085A-498	Sequence 498, App	2
44	36	49.3	1041	3	US-10-145-129A-498	Sequence 498, App	
45	36	49.3	1041	3	US-10-013-929A-498	Sequence 498, App	
46	36	49.3	1041	3	US-10-013-917A-498	Sequence 498, App	
47	36	49.3	1059	2	US-09-954-987B-187	Sequence 187, App	
48	36	49.3	1181	1	US-08-053-614-4	Sequence 4, Appl:	
49	36	49.3	1181	1	US-08-316-397B-4	Sequence 4, Appli	
50	36	49.3	1181	_	US-09-034-306-4	Sequence 4, Appl:	
			1181	1			
51	36	49.3		2	US-09-259-437-4	Sequence 4, Appl:	
52	36	49.3	1181	5	PCT-US93-09782-4	Sequence 4, Appl:	
53	35	47.9	80	2	US-09-248-796A-25415	Sequence 25415, A	
54	35	47.9	187	2	US-09-248-796A-19489	Sequence 19489, A	
55	35	47.9	218	2	US-09-489-039A-13787	Sequence 13787, 1	
56	35	47.9	404	2	US-09-242-859A-11	Sequence 11, App.	
57	35	47.9	405	2	US-09-538-092-1059	Sequence 1059, Ap	
58	35	47.9	416	2	US-09-949-016-7485	Sequence 7485, Ap	
59	35	47.9	448	2	US-09-902-540-16109	Sequence 16109, A	4
60	35	47.9	765	2	US-09-543-681A-4287	Sequence 4287, Ap	c
61	35	47.9	792	2	US-09-248-796A-18842	Sequence 18842, I	
62	35	47.9	824	2	US-10-055-364-43	Sequence 43, App.	
63	35	47.9	874	2	US-08-804-439A-16	Sequence 16, App.	
			ŕ				

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-15.r

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 15.rapbm.

start

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:29:53; Search time 75.9934 Seconds

(without alignments)

91.432 Million cell updates/sec

US-10-001-938-15 Title:

Perfect score: 73

Sequence: 1 FRSVSTSTTFVQGRR 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2097797 segs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:* 6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	73	100.0		_	US-10-001-938-15	Sequence 15, Appl
2	49	67.1	-		US-10-264-049-2674	Sequence 2674, Ap
3	44	60.3	92	5	US-10-450-763-58559	Sequence 58559, A

4	44	60.3	164	4	US-10-363-829-341	Somiones 241 App
4 5	44	60.3	227	4	US-10-363-629-341 US-10-220-120-322	Sequence 341, App
				-		Sequence 322, App
6	43	58.9	85	4	US-10-425-115-242949	Sequence 242949,
7	43	58.9	97	4	US-10-425-115-246113	Sequence 246113,
8	42	57.5	1473	4	US-10-437-963-111000	Sequence 111000,
9	41	56.2	52	4	US-10-425-115-210546	Sequence 210546,
10	41	56.2	326	6	US-11-096-568A-7817	Sequence 7817, Ap
11	41	56.2	328	6	US-11-096-568A-7816	Sequence 7816, Ap
12	40	54.8	83	5	US-10-617-320-4269	Sequence 4269, Ap
13	40	54.8	108	5	US-10-617-320-5049	Sequence 5049, Ap
14	40	54.8	843	4	US-10-156-761-13999	Sequence 13999, A
15	40	54.8	843	5	US-10-732-923-1579	Sequence 1579, Ap
16	39	53.4	80	4	US-10-424-599-273144	Sequence 273144,
17	39	53.4	123	4	US-10-437-963-122175	Sequence 122175,
18	39	53.4	509	4	US-10-074-978A-204	Sequence 204, App
19	39	53.4	509	4	US-10-074-978A-205	Sequence 205, App
20	39	53.4	509	4	US-10-074-978A-206	Sequence 206, App
21	39	53.4	513	5	US-10-732-923-1992	Sequence 1992, Ap
22	39	53.4	529	4	US-10-437-963-125175	Sequence 125175,
23	39	53.4	591	5	US-10-450-763-48382	Sequence 48382, A
24	38	52.1	325	4	US-10-282-122A-45976	Sequence 45976, A
25	38	52.1	339	4	US-10-104-047-2843	Sequence 2843, Ap
26	38	52.1	339	6	US-11-072-512-2843	
						Sequence 2843, Ap
27	38	52.1	396	3	US-09-925-301-852	Sequence 852, App
28	38	52.1	432	4	US-10-264-049-2915	Sequence 2915, Ap
29	38	52.1	540	4	US-10-104-047-3747	Sequence 3747, Ap
30	38	52.1	540	6	US-11-072-512-3747	Sequence 3747, Ap
31	38	52.1	582	5	US-10-635-407-16	Sequence 16, Appl
32	38	52.1	622	5	US-10-635-407-138	Sequence 138, App
33	38	52.1	623	4	US-10-116-275-144	Sequence 144, App
34	38	52.1	623	5	US-10-753-267-10	Sequence 10, Appl
35	38	52.1	623	5	US-10-756-149-5040	Sequence 5040, Ap
36	38	52.1	623	5	US-10-635-407-8	Sequence 8, Appli
37	38	52.1	623	5	US-10-635-407-112	Sequence 112, App
38	38	52.1	623	5	US-10-635-407-114	Sequence 114, App
39	38	52.1	623	5	US-10-635-407-116	Sequence 116, App
40	38	52.1	623	5	US-10-635-407-118	Sequence 118, App
41	38	52.1	623	5	US-10-635-407-120	Sequence 120, App
42	38	52.1	623	5	US-10-635-407-122	Sequence 122, App
43	38	52.1	623	5	US-10-635-407-124	Sequence 124, App
44	38	52.1	623	5	US-10-635-407-126	Sequence 126, App
45	38	52.1	623	5	US-10-635-407-128	Sequence 128, App
46	38	52.1	623	5	US-10-635-407-130	Sequence 130, App
47	38	52.1	623	5	US-10-635-407-132	Sequence 132, App
48	38	52.1	623	5	US-10-635-407-134	Sequence 134, App
49	38	52.1	623	5	US-10-635-407-136	Sequence 136, App
50	38	52.1	623	5	US-10-635-407-140	Sequence 140, App
51	38	52.1	623	5	US-10-635-407-142	Sequence 142, App
52	38	52.1	623	5	US-10-635-407-144	Sequence 144, App
53	38	52.1	623	5	US-10-635-407-146	Sequence 146, App
54	38	52.1	623	5	US-10-635-407-148	Sequence 148, App
55	38	52.1	623	5	US-10-635-407-140	Sequence 150, App
56 57	38	52.1	623 623	5 5	US-10-635-407-152	Sequence 152, App
	38	52.1			US-10-635-407-154	Sequence 154, App
58	38	52.1	623	5	US-10-878-556A-62	Sequence 62, Appl
59 60	38	52.1	627	5	US-10-635-407-12	Sequence 12, Appl
60	38	52.1	627	5	US-10-635-407-14	Sequence 14, Appl
61	38	52.1	628	5	US-10-635-407-10	Sequence 10, Appl
62	37	50.7	58	4	US-10-291-265-317	Sequence 317, App
63	37	50.7	58	6	US-11-000-463-317	Sequence 317, App
64	37	50.7	70	4	US-10-425-115-234142	Sequence 234142,

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-15.rapbn.

Score Home Retrieve Application **SCORE System SCORE** Comments / Page List FAQ Suggestions Overview

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-15.rapbn.

start

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title: US-10-001-938-15

Perfect score: 73

1 FRSVSTSTTFVQGRR 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

> /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:* /EMC_Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	73	100.0	15	6	US-10-490-949-24	Sequence 24, Appl
2	37	50.7	150	6	US-10-953-349-38479	Sequence 38479, A
3	36	49.3	164	6	US-10-953-349-36632	Sequence 36632, A
4	36	49.3	312	6	US-10-953-349-20709	Sequence 20709, A
5	36	49.3	413	6	US-10-953-349-7374	Sequence 7374, Ap
6	36	49.3	445	6	US-10-953-349-7373	Sequence 7373, Ap
7	36	49.3	483	6	US-10-953-349-7372	Sequence 7372, Ap
8	34	46.6	136	7	US-11-293-697-4484	Sequence 4484, Ap
9	34	46.6	272	7	US-11-293-697-4608	Sequence 4608, Ap
10	34	46.6	325	6	US-10-953-349-8881	Sequence 8881, Ap
11	34	46.6	331	6	US-10-953-349-8880	Sequence 8880, Ap
12	34	46.6	342	6	US-10-953-349-8879	Sequence 8879, Ap
13	34 33	46.6 45.2	838 126	7	US-11-295-336-2	Sequence 2, Appli
14 15	33	45.2	126	6 6	US-10-953-349-17379 US-10-953-349-23925	Sequence 17379, A
16	33	45.2	134	6	US-10-953-349-23925 US-10-953-349-17378	Sequence 23925, A Sequence 17378, A
17	33	45.2	134	6	US-10-953-349-17376	Sequence 23924, A
18	33	45.2	134	6	US-10-953-349-26245	Sequence 26245, A
19	33	45.2	137	6	US-10-953-349-28995	Sequence 28995, A
20	33	45.2	160	6	US-10-953-349-17377	Sequence 17377, A
21	33	45.2	160	6	US-10-953-349-23923	Sequence 23923, A
22	33	45.2	195	6	US-10-953-349-31424	Sequence 31424, A
23	33	45.2	197	6	US-10-953-349-15564	Sequence 15564, A
24	33	45.2	200	6	US-10-953-349-10713	Sequence 10713, A
25	33	45.2	211	6	US-10-953-349-31423	Sequence 31423, A
26	33	45.2	236	6	US-10-953-349-31422	Sequence 31422, A
27	33	45.2	4373	7	US-11-118-524-2	Sequence 2, Appli
28	32	43.8	159	7	US-11-122-986-221	Sequence 221, App
29	32	43.8	159	7	US-11-122-986-223	Sequence 223, App
30	32	43.8	211	6	US-10-953-349-4200	Sequence 4200, Ap
31	32	43.8	215	7	US-11-249-111-95	Sequence 95, Appl
32	32	43.8	246	6	US-10-953-349-4199	Sequence 4199, Ap
33	32	43.8	255	6	US-10-953-349-7139	Sequence 7139, Ap
34	32	43.8	258	6	US-10-953-349-7138	Sequence 7138, Ap
35 36	32 32	43.8 43.8	272 272	6 6	US-10-953-349-4198 US-10-953-349-13203	Sequence 4198, Ap Sequence 13203, A
37	32	43.8	288	6	US-10-953-349-13202	Sequence 13203, A
38	32	43.8	310	6	US-10-953-349-13202	Sequence 13202, A
39	32	43.8	314	6	US-10-953-349-28317	Sequence 28317, A
40	32	43.8	371	6	US-10-953-349-28316	Sequence 28316, A
41	32	43.8	433		US-10-953-349-7137	Sequence 7137, Ap
42	32	43.8	632	6	US-10-953-349-12946	Sequence 12946, A
43	32	43.8	635	6	US-10-953-349-12945	Sequence 12945, A
44	32	43.8	644	6	US-10-953-349-12944	Sequence 12944, A
45	32	43.8	1033	7	US-11-121-154-207	Sequence 207, App
46	31	42.5	109	7	US-11-254-679-9	Sequence 9, Appli
47	31	42.5	122	6	US-10-953-349-20387	Sequence 20387, A
48	31	42.5	148	6	US-10-953-349-20385	Sequence 20385, A
49	31	42.5	162	6	US-10-953-349-30554	Sequence 30554, A
50	31	42.5	175	6	US-10-953-349-33661	Sequence 33661, A
51	31	42.5	177		US-10-953-349-16399	Sequence 16399, A
52 53	31	42.5	179	6	US-10-953-349-30553	Sequence 30553, A
53 54	31	42.5	184	6	US-10-953-349-16398	Sequence 16398, A
54 55	31	42.5	184	6	US-10-953-349-33660	Sequence 33660, A
55 56	31 31	42.5 42.5	203 217	6 6	US-10-953-349-30552 US-10-953-349-23578	Sequence 30552, A
57	31	42.5	217	6	US-10-953-349-23577	Sequence 23578, A Sequence 23577, A
58	31	42.5	256		US-10-953-349-23576	Sequence 23576, A
59	31	42.5	256		US-10-953-349-39697	Sequence 39697, A
		-2.5		•		2242222 2227/ 11

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-16.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 16.rai.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:08:52; Search time 11.4238 Seconds

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-16

Perfect score: 82

Sequence: 1 PGMVQQIQSVCMECQ 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description		
1	82	100.0	397	1	US-08-868-288A-5	Sequence 5, Appli		
2	82	100.0	397	2	US-09-235-373-5	Sequence 5, Appli		

_				_		
3	82	100.0	397	2	US-09-388-993-5	Sequence 5, Appli
4	82	100.0	397	2	US-09-919-039-178	Sequence 178, App
5	82	100.0	397	2	US-09-538-092-1052	Sequence 1052, Ap
6	82	100.0	397	2	US-09-501-714-5	Sequence 5, Appli
7	71	86.6	239	2	US-10-104-047-2162	Sequence 2162, Ap
8	71	86.6	397	3	US-10-429-223-2	Sequence 2, Appli
9	71	86.6	397	3	US-10-429-223-4	Sequence 4, Appli
10	51	62.2	419	1	US-08-686-417-3	Sequence 3, Appli
11	50	61.0	330	2	US-09-248-796A-19977	Sequence 19977, A
12	49	59.8	459	1	US-08-870-518-4	Sequence 4, Appli
13	45	54.9	397	2	US-09-248-796A-17628	Sequence 17628, A
14	45	54.9	486	1	US-08-870-518-3	Sequence 3, Appli
15	44	53.7	345	2	US-09-248-796A-14816	Sequence 14816, A
16	42	51.2	492	2	US-09-107-532A-6385	Sequence 6385, Ap
17	40	48.8	273	2	US-09-248-796A-17627	Sequence 17627, A
18	39	47.6	114	2	US-09-865-483-8	Sequence 8, Appli
19	39	47.6	114	2	US-10-726-555-8	Sequence 8, Appli
20	39	47.6	116	2	US-08-397-411-4	Sequence 4, Appli
21	39	47.6	119	1	US-07-634-278-60	Sequence 60, Appl
22	39	47.6	119	1	US-08-477-728-60	Sequence 60, Appl
			119			
23	39	47.6		1	US-08-474-040-60	Sequence 60, Appl
24	39	47.6	119	1	US-08-487-200-60	Sequence 60, Appl
25	39	47.6	119	2	US-08-484-537-60	Sequence 60, Appl
26	39	47.6	119	3	US-09-718-998-60	Sequence 60, Appl
27	39	47.6	124	2	US-09-270-767-48315	Sequence 48315, A
28	39	47.6	138	1	US-07-634-278-33	Sequence 33, Appl
29	39	47.6	138	1	US-08-477-728-33	Sequence 33, Appl
30	39	47.6	138	1	US-08-474-040-33	Sequence 33, Appl
31	39	47.6	138	1	US-08-487-200-33	Sequence 33, Appl
32	39	47.6	138	2	US-08-484-537-33	Sequence 33, Appl
33	39	47.6	138	3	US-09-718-998-33	Sequence 33, Appl
34	39	47.6	234	2	US-09-040-483-5	Sequence 5, Appli
35	39	47.6	234	2	US-08-740-036-5	Sequence 5, Appli
36	39	47.6	234	3	US-09-645-399-5	Sequence 5, Appli
37	39	47.6	282	2	US-10-104-047-2824	Sequence 2824, Ap
38	39	47.6	470	2	US-10-104-047-3177	Sequence 3177, Ap
39	39	47.6	478	2	US-09-770-916-2	Sequence 2, Appli
40	39	47.6	582	1	US-08-989-386-1	Sequence 1, Appli
41	39	47.6	588	2	US-10-094-749-2309	Sequence 2309, Ap
42	38.5	47.0	362	2	US-09-252-991A-18068	Sequence 18068, A
43		47.0		2		Sequence 294, App
44	38.5	47.0	1917	2	US-09-949-002-485	Sequence 485, App
45	38	46.3	85	2	US-09-263-933-6	Sequence 6, Appli
46	38	46.3	85	2	US-09-263-933-13	Sequence 13, Appl
47	38	46.3	85	2	US-09-263-933-20	Sequence 20, Appl
48	38	46.3	85	2	US-09-919-901-6	Sequence 6, Appli
49	38	46.3	85	2	US-09-919-901-13	Sequence 13, Appl
50	38	46.3	85	2	US-09-919-901-20	Sequence 20, Appl
51	38	46.3	85	2	US-10-191-966-6	Sequence 6, Appli
52	38	46.3	85	2	US-10-191-966-13	Sequence 13, Appl
53	38	46.3	85	2	US-10-191-966-20	Sequence 20, Appl
54	38	46.3	228	2	US-10-104-047-2483	Sequence 2483, Ap
55	38	46.3	243	2	US-09-469-242-2	Sequence 2, Appli
56	38	46.3	328	2	US-09-350-702-16	Sequence 16, Appl
57	38	46.3	680	2	US-09-538-092-1165	Sequence 1165, Ap
					US-09-949-016-6637	
58 50	38	46.3	680	2		Sequence 6637, Ap
59 60	38	46.3	708	2	US-09-949-016-6638	Sequence 6638, Ap
60	38	46.3	712	2	US-09-949-016-7340	Sequence 7340, Ap
61	. 38	46.3	712	2	US-09-949-016-7341	Sequence 7341, Ap
62	38	46.3	2307	2	US-09-263-933-2	Sequence 2, Appli
63	38	46.3	2307	2	US-09-263-933-9	Sequence 9, Appli

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 16.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 16.rapbm.

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OM protein - protein search, using sw model

June 2, 2006, 19:29:53; Search time 75.9934 Seconds Run on:

(without alignments)

91.432 Million cell updates/sec

US-10-001-938-16 Title:

Perfect score: 82

Sequence: 1 PGMVQQIQSVCMECQ 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

2097797 segs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA Main:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

> 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	82	100.0	15	4	US-10-001-938-16	Sequence 16, Appl

						_	
2	82	100.0	165	4	US-10-106-698-6762	Sequence	6762, Ap
3	82	100.0	165	5	US-10-473-127-1142	Sequence	1142, Ap
4	82	100.0	252	4	US-10-264-049-4191	Sequence	4191, Ap
5	82	100.0	258	5	US-10-473-127-1141	Sequence	· -
6	82		258	5	US-10-473-127-1146		
		100.0				Sequence	_
7	82	100.0	397	3	US-09-919-039-178	Sequence	
8	82	100.0	397	5	US-10-473-127-1138	Sequence	1138, Ap
9	82	100.0	397	5	US-10-473-127-1139	Sequence	1139, Ap
10	82	100.0	397	5	US-10-473-127-1140	Sequence	1140, Ap
11	82	100.0	397	5	US-10-473-127-1143	Sequence	
12	82	100.0	397	5	US-10-473-127-1144	Sequence	
						-	
13	82	100.0	397	5	US-10-473-127-1145	Sequence	
14	82	100.0	397	5	US-10-756-149-4727	Sequence	
15	82	100.0	397	5	US-10-631-467-559	Sequence	559, App
16	82	100.0	397	5	US-10-631-467-1386	Sequence	1386, Ap
17	82	100.0	397	5	US-10-878-556A-155	Sequence	_
18	82	100.0	408	5	US-10-450-763-40099		40099, A
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20	71	86.6	239	4	US-10-104-047-2162	Sequence	_
21	71	86.6	239	6	US-11-072-512-2162	Sequence	
22	71	86.6	397	4	US-10-108-260A-3837	Sequence	3837, Ap
23	71	86.6	397	4	US-10-429-223-2	Sequence	2, Appli
24	71	86.6	397	4	US-10-429-223-4	Sequence	
25	71	86.6	426	4	US-10-108-260A-4751	Sequence	
26	65	79.3	412	5	US-10-965-898-18	_	18, Appl
27	65	79.3	479	4	US-10-788-792-186	-	186, App
28	59	72.0	244	4	US-10-425-115-217751	Sequence	217751,
29	59	72.0	420	4	US-10-767-701-46164	Sequence	46164, A
30	57	69.5	363	4	US-10-425-115-304214	Sequence	304214,
31	56	68.3	211	4	US-10-767-701-47401	-	47401, A
32	56	68.3	330	6	US-11-096-568A-16062	_	16062, A
33	56	68.3	336	6	US-11-096-568A-16061	_	
				_		-	16061, A
34	56	68.3	370	4	US-10-259-194A-44	Sequence	
35	56	68.3	417	4	US-10-437-963-194306	Sequence	
36	56	68.3	417	4	US-10-425-115-307680	Sequence	307680,
37	56	68.3	418	4	US-10-425-115-307678	Sequence	307678,
38	56	68.3	418	4	US-10-425-115-307679	Sequence	307679,
39	56	68.3	433	4	US-10-425-114-60908	_	60908, A
40	52	63.4	217	4	US-10-424-599-271036	Sequence	
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42		63.4	398	4	US-10-425-114-55344		55344, A
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44	52	63.4	416	4	US-10-437-963-188385	Sequence	188385,
45	52	63.4	417	4	US-10-424-599-271037	Sequence	271037,
46	52	63.4	420	4	US-10-424-599-257607	Sequence	257607,
47	52	63.4	420	4	US-10-424-599-257608	Sequence	
48	52	63.4	420	4	US-10-437-963-128712	Sequence	
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49	52	63.4	422	4	US-10-425-115-332061	Sequence	
50	52	63.4	424	4	US-10-425-114-46242		46242, A
51	52	63.4	433	4	US-10-425-114-63266	Sequence	63266, A
52	52	63.4	435	4	US-10-425-114-59462	Sequence	59462, A
53	52	63.4	435	4	US-10-425-114-65366	Sequence	65366, A
54	51	62.2	338	6	US-11-096-568A-21865		21865, A
55	51	62.2	342	4	US-10-425-114-68558	-	68558, A
56	51	62.2	419	4	US-10-437-963-194308	Sequence	
						_	
57	51	62.2	419	4	US-10-767-701-47403		47403, A
58	51	62.2	419	4	US-10-425-115-266771	Sequence	
59	51	62.2	419	4	US-10-425-115-266773	Sequence	
60	51	62.2	419	4	US-10-425-115-266781	Sequence	266781,
61	51	62.2	419	4	US-10-425-115-305086	Sequence	305086,
62	51	62.2	419	6	US-11-096-568A-21864	_	21864, A
	_	_				•	,

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-16.rapbn.

Score Home Page **Retrieve Application**

List

SCORE System Overview

SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 938-16.rapbn.

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title: US-10-001-938-16

Perfect score: 82

Sequence: 1 PGMVQQIQSVCMECQ 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result Query

No.	Score	Match	Length	DB	ID	Description
1	82	100.0	15	6	US-10-490-949-25	Sequence 25, Appl
2	71	86.6	397	7	US-11-293-697-3837	Sequence 3837, Ap
3	71	86.6	426	7	US-11-293-697-4751	Sequence 4751, Ap
4	55	67.1	257	6	US-10-953-349-1056	Sequence 1056, Ap
5	55	67.1	337	6	US-10-953-349-1055	Sequence 1055, Ap
6	55	67.1	419	6	US-10-953-349-1054	Sequence 1054, Ap
7	52	63.4	338	6	US-10-953-349-13711	Sequence 13711, A
8	52	63.4	382 420	6 6	US-10-953-349-13710	Sequence 13710, A Sequence 13709, A
9 10	52 50	63.4 61.0	256	6	US-10-953-349-13709 US-10-953-349-16379	Sequence 13709, A
11	50	61.0	336	6	US-10-953-349-16378	Sequence 16378, A
12	50	61.0	417	6	US-10-953-349-16377	Sequence 16377, A
13	39	47.6	63	6	US-10-953-349-27957	Sequence 27957, A
14	38.5	47.0	1822	6	US-10-505-928-700	Sequence 700, App
15	38	46.3	708	6	US-10-505-928-416	Sequence 416, App
16	37	45.1	171	6	US-10-953-349-36964	Sequence 36964, A
17	37	45.1	183	6	US-10-953-349-36963	Sequence 36963, A
18	37	45.1	206	6	US-10-953-349-35898	Sequence 35898, A
19	37	45.1	234	6	US-10-505-928-152	Sequence 152, App
20	37	45.1	246	6	US-10-953-349-35897	Sequence 35897, A
21	37	45.1	300	6	US-10-953-349-35896	Sequence 35896, A
22	36	43.9	112	7 7	US-11-293-697-3203	Sequence 3203, Ap
23 24	36 36	43.9 43.9	117 146	7	US-11-219-121-11 US-11-219-121-13	Sequence 11, Appl Sequence 13, Appl
25	36	43.9	341	6	US-10-953-349-17124	Sequence 17, Appr Sequence 17124, A
26	36	43.9	352	6	US-10-953-349-17123	Sequence 17124, A
27	36	43.9	437	6	US-10-953-349-17122	Sequence 17122, A
28	36	43.9	790	6	US-10-511-937-2937	Sequence 2937, Ap
29	35	42.7	141	7	US-11-293-697-2640	Sequence 2640, Ap
30	35	42.7	420	7	US-11-232-370-7	Sequence 7, Appli
31	35	42.7	524	7	US-11-232-370-12	Sequence 12, Appl
32	35	42.7	525	7	US-11-232-370-13	Sequence 13, Appl
33	35	42.7	525	7	US-11-232-370-14	Sequence 14, Appl
34	35	42.7	543	7	US-11-232-370-6	Sequence 6, Appli
35	35	42.7	544	7	US-11-232-370-9	Sequence 9, Appli
36	35	42.7	544	7	US-11-232-370-11	Sequence 11, Appl
37	35	42.7	545	7 7	US-11-232-370-8	Sequence 8, Appli
38	35	42.7	559 660	_	US-11-232-370-10	Sequence 10, Appl
39 40	35 34	42.7 41.5	660 25	6 7	US-10-953-349-10967 US-11-219-563-115	Sequence 10967, A Sequence 115, App
41	34	41.5	82	7	US-11-219-563-119	Sequence 119, App
42	34	41.5	91	6	US-10-514-263-7	Sequence 7, Appli
43	34	41.5	108	7	US-11-328-747-6	Sequence 6, Appli
44	34	41.5	109	6	US-10-953-349-7536	Sequence 7536, Ap
45	34	41.5	118	6	US-10-953-349-7535	Sequence 7535, Ap
46	34	41.5	118	6	US-10-506-063A-14	Sequence 14, Appl
47	34	41.5	119		US-10-953-349-39848	Sequence 39848, A
48	34	41.5	119		US-10-953-349-39911	Sequence 39911, A
49	34	41.5	121	7	US-11-219-563-84	Sequence 84, Appl
50	34	41.5	121		US-11-219-563-89	Sequence 89, Appl
51 52	34	41.5	121	7	US-11-219-563-90	Sequence 90, Appl
52 53	34	41.5 41.5	125	6	US-10-953-349-29673	Sequence 29673, A
53 54	34 34	41.5	143 145		US-10-953-349-39847 US-10-953-349-39909	Sequence 39847, A Sequence 39909, A
55	34	41.5	153		US-10-953-349-29671	Sequence 29671, A
56	34	41.5	164	6	US-10-953-349-12472	Sequence 12472, A
57	34	41.5	196		US-10-953-349-12471	Sequence 12471, A
58	34	41.5	202		US-10-953-349-16651	Sequence 16651, A
59	34	41.5	230		US-10-953-349-32248	Sequence 32248, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-17.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 17.rai.

start

Go Back to previc

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:08:52; Search time 11.4238 Seconds Run on:

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-17

Perfect score: 76

1 GRRITTRRIMENGQE 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents AA:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* 7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length DB I		ID	Description		
1 2		100.0			US-08-868-288A-7 US-09-235-373-7	Sequence 7, Appli Sequence 7, Appli		

•	7.0	100 0	077	^	00 200 002 7	a	7 71:
3	76	100.0	277	2	US-09-388-993-7		7, Appli
4	76	100.0	277	2	US-09-501-714-7		7, Appli
5	76	100.0	327	2	US-09-949-016-11262	-	11262, A
6	76	100.0	351	1	US-08-868-288A-6	Sequence	6, Appli
7	76	100.0	351	2	US-09-235-373-6	Sequence	6, Appli
8	76	100.0	351	2	US-09-388-993-6	Sequence	6, Appli
9	76	100.0	351	2	US-09-501-714-6		6, Appli
10	66	86.8	330	1	US-08-868-288A-3	_	3, Appli
11	66	86.8	330	2	US-09-235-373-3		3, Appli
12	66	86.8	330	2	US-09-388-993-3		3, Appli
						_	
13	66	86.8	330	2	US-09-501-714-3	_	3, Appli
14	45	59.2	379	2	US-09-967-552A-2		2, Appli
15	45	59.2	379	2	US-09-967-552A-26		26, Appl
16	45	59.2	379	2	US-09-967-552A-30	_	30, Appl
17	45	59.2	391	2	US-09-967-552A-18	_	18, Appl
18	41	53.9	405	2	US-09-134-000C-4680	Sequence	4680, Ap
19	41	53.9	867	2	US-09-668-673B-2	Sequence	2, Appli
20	41	53.9	867	2	US-10-389-532-2	Sequence	2, Appli
21	41	53.9	1558	2	US-09-949-016-6803	_	6803, Ap
22	41	53.9	1606	2	US-09-949-016-7371	-	7371, Ap
23	40	52.6	207	2	US-09-248-796A-15834		15834, A
24	40	52.6	268	2	US-09-270-767-44519	_	44519, A
						_	
25	39	51.3	178	2	US-09-107-532A-3960		3960, Ap
26	39	51.3	184	2	US-09-198-452A-1138		1138, Ap
27	39	51.3	315	2	US-09-438-185A-26	-	26, Appl
28	38	50.0	130	2	US-09-489-039A-11337	_	11337, A
29	38	50.0	165	2	US-09-902-540-15997		15997, A
30	38	50.0	414	2	US-09-252-991A-27975	Sequence	27975, A
31	38	50.0	455	2	US-09-902-540-11484	Sequence	11484, A
32	38	50.0	473	2	US-09-489-039A-9737	Sequence	9737, Ap
33	38	50.0	764	2	US-09-585-858-15	Sequence	15, Appl
34	38	50.0	764	2	US-10-270-878-15	_	15, Appl
35	38	50.0	837	1	US-08-680-326-117		117, App
36	38	50.0	1008	1	US-08-680-326-30		30, Appl
37	38	50.0	1009	1	US-08-680-326-31		31, Appl
				2			
38	38	50.0	1037		US-09-902-540-9845		9845, Ap
39	38	50.0	1341	2	US-09-252-991A-26785	-	26785, A
40	37	48.7	375	2	US-09-303-518D-632		632, App
41	37	48.7	375	2	US-09-303-518D-634	_	634, App
42	37	48.7	544	2	US-09-252-991A-28995		28995, A
43	36	47.4	92	2	US-09-902-540-13452	-	13452, A
44	36	47.4	165	2	US-09-252-991A-31768	Sequence	31768, A
45	36	47.4	233	2	US-09-489-039A-9119	Sequence	9119, Ap
46	36	47.4	301	2	US-09-252-991A-22565	Sequence	22565, A
47	36	47.4	314	2	US-09-252-991A-26728	Sequence	26728, A
48	36	47.4	355	2	US-09-328-352-6270		6270, Ap
49	36	47.4	498	2	US-09-477-962-114		114, App
50	36	47.4	610	2	US-09-248-796A-17030	-	17030, A
51	36	47.4	636	2	US-09-489-039A-13947	_	13947, A
				2	US-09-371-338-15		15, Appl
52	36	47.4	651			_	
53	36	47.4	703	2	US-10-116-326-6		6, Appli
54	36	47.4	703	2	US-10-803-277-6		6, Appli
55	36	47.4	762	2	US-10-116-326-4		4, Appli
56	36	47.4	762	2	US-10-803-277-4		4, Appli
57	36	47.4	778	2	US-10-116-326-2		2, Appli
58	36	47.4	778	2	US-10-003-690-2	-	2, Appli
59	36	47.4	778	2	US-10-803-277-2	_	2, Appli
60	36	47.4	898	1	US-08-465-995A-4	Sequence	4, Appli
61	36	47.4	898	1	US-08-465-994C-4	Sequence	4, Appli
62	36	47.4	898	1	US-08-966-145-4		4, Appli
63	36	47.4	920	1	US-08-101-593-4		4, Appli
		- · · ·		_		•	

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-17.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 17.rapbm.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:29:53; Search time 75.9934 Seconds

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-17

Perfect score: 76

Sequence: 1 GRRITTRRIMENGQE 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용 Result Query No. Score Match Length DB ID Description ------76 100.0 15 4 US-10-001-938-17 Sequence 17, Appl

2	66	86.8	242	4	US-10-264-049-2674	Sequence	2674, Ap
3	63	82.9	164	4	US-10-363-829-341	Sequence	341, App
4	63	82.9	227	4	US-10-220-120-322	Sequence	
5	60	78.9	232	5	US-10-480-988-22	Sequence	
6	60	78.9	267	3	US-09-764-868-1164	_	1164, Ap
						•	
7	60	78.9	267	3	US-09-764-891-4089	Sequence	
8	45	59.2	338	6	US-11-188-298-15117		15117, A
9	45	59.2	379	3	US-09-967-552A-2	Sequence	
10	45	59.2	379	3	US-09-967-552A-26	Sequence	26, Appl
11	45	59.2	379	3	US-09-967-552A-30	Sequence	30, Appl
12	45	59.2	379	5	US-10-965-357-2	Sequence	
13	45	59.2	379	5	US-10-965-357-26	Sequence	
14	45	59.2	379	5	US-10-965-357-30	Sequence	
15	45	59.2	379	5	US-10-967-851-2	Sequence	
16	45	59.2	379	5	US-10-967-851-26	Sequence	
17	45	59.2	379	5	US-10-967-851-30	Sequence	30, Appl
18	45	59.2	379	6	US-11-188-298-9209	Sequence	9209, Ap
19	45	59.2	379	6	US-11-188-298-12077		12077, A
20	45	59.2	379	6	US-11-188-298-13625	-	13625, A
21	45	59.2	379	6	US-11-188-298-17015	-	17015, A
				-	US-09-906-549-2		
22	45	59.2	380	3	•		2, Appli
23	45	59.2	380	6	US-11-188-298-2231	-	2231, Ap
24	45	59.2	380	6	US-11-188-298-15608	Sequence	15608, A
25	45	59.2	388	4	US-10-425-115-347505	Sequence	347505,
26	45	59.2	391	3	US-09-967-552A-18	Sequence	18, Appl
27	45	59.2	391	5	US-10-965-357-18	Sequence	18, Appl
28	45	59.2	391	5	US-10-967-851-18	-	18, Appl
29	45	59.2	443	5	US-10-739-930-8161		8161, Ap
30	45	59.2	453	4	US-10-425-114-65489	_	
				_		-	65489, A
31	44	57.9	379	4	US-10-767-701-44558		44558, A
32	43	56.6	137	4	US-10-437-963-156565	Sequence	
33	43	56.6	143	4	US-10-425-115-337503	Sequence	
34	43	56.6	375	4	US-10-424-599-271970	Sequence	271970,
35	42	55.3	78	4	US-10-425-115-290387	Sequence	290387,
36	42	55.3	202	4	US-10-425-114-47897	Sequence	47897, A
37	42	55.3	427	4	US-10-425-114-45447	-	45447, A
38	42	55.3	563	4	US-10-425-115-286927	Sequence	
39	42	55.3	568	4	US-10-425-115-263963	Sequence	
						-	
40	42	55.3	591	4	US-10-425-114-61059	_	61059, A
41	42	55.3	699	4	US-10-437-963-192225	Sequence	
42	42	55.3	2391	4	US-10-425-115-245853	Sequence	
43	41	53.9	77	3	US-09-989-890-171		171, App
44	41	53.9	98	4	US-10-437-963-202081	Sequence	202081,
45	41	53.9	867	4	US-10-389-532-2	Sequence	2, Appli
46	41	53.9	1845	4	US-10-408-765A-1351	Sequence	1351, Ap
47	40	52.6	264	6	US-11-097-143-42933	Sequence	42933, A
48	40	52.6	404	4	US-10-437-963-117500	Sequence	
49	40	52.6	416	4	US-10-425-114-65332		65332, A
50	40	52.6	625	5	US-10-739-930-5867		5867, Ap
51	40	52.6	1061	4	US-10-369-493-12847		12847, A
52	40	52.6	8805	6	US-11-097-143-28128		28128, A
53	39	51.3	38	4	US-10-425-115-242521	Sequence	
54	39	51.3	92	4	US-10-437-963-113613	Sequence	113613,
55	39	51.3	108	4	US-10-767-701-34584	Sequence	34584, A
56	39	51.3	184	4	US-10-289-762-1138	Sequence	1138, Ap
57	39	51.3	191	3	US-09-733-507-2	_	2, Appli
58	39	51.3	210	4	US-10-424-599-203088	Sequence	
59	39	51.3	456	4	US-10-425-114-51670		51670, A
60	39	51.3	671	4			76971, A
					US-10-282-122A-76971		
61	39	51.3	773	4	US-10-437-963-121782	Sequence	
62	39	51.3	1450	4	US-10-437-963-110511	Sequence	110211,

SCORE Search Results Details for Application 10 and Search Result us-10-001-938-17.rapb

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 start

Go Bac

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OM protein - protein search, using sw model

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title: US-10-001-938-17

Perfect score: 76

Sequence: 1 GRRITTRRIMENGQE 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

58871 segs, 11565156 residues Searched:

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA New:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

> 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:* 7: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1 2	76 41	100.0	15 867	6 7	US-10-490-949-26 US-11-316-132-3	Sequence 26, Appl Sequence 3, Appli

_				_	44 054 704 00	_	
3	36	47.4	18	7	US-11-251-734-28		28, Appl
4	36	47.4	174	6	US-10-953-349-28370	•	28370, A
5	35	46.1	166	6	US-10-953-349-30966	Sequence	30966, A
6	35	46.1	212	6	US-10-953-349-30965	Sequence	30965, A
7	35	46.1	289	7	US-11-293-697-4302	Sequence	4302, Ap
8	35	46.1	293	6	US-10-953-349-30964	Sequence	30964, A
9	35	46.1	870	7	US-11-316-132-4	Sequence	4, Appli
10	34	44.7	207	6	US-10-953-349-28505		28505, A
11	34	44.7	233	6	US-10-953-349-28504		28504, A
12	34	44.7	336	6	US-10-953-349-28503		28503, A
13	34	44.7	355	6	US-10-953-349-19922		19922, A
14	34	44.7	362	6	US-10-511-937-2509		2509, Ap
15	34	44.7	363	6	US-10-953-349-19921		19921, A
16	34	44.7	365	6	US-10-511-937-2530		2530, Ap
17	34	44.7	372	7	US-11-319-606-3		3, Appli
18	34	44.7	381	6	US-10-953-349-19920		19920, A
19	33	43.4	154	6	US-10-953-349-33149	Sequence	33149, A
20	33	43.4	362	6	US-10-953-349-26895	Sequence	26895, A
21	33	43.4	375	6	US-10-953-349-26894	Sequence	26894, A
22	33	43.4	619	7	US-11-312-958-46	Sequence	46, Appl
23	33	43.4	730	6	US-10-505-928-841		841, App
24	33	43.4	870	7	US-11-316-132-2		2, Appli
25	33	43.4	871	7	US-11-316-132-1	<u>-</u>	1, Appli
26	32.5	42.8	985	7	US-11-342-171-6	-	6, Appli
27				7	US-11-342-171-66		
	32.5	42.8	985				66, Appl
28	32	42.1	212	6	US-10-953-349-5598	_	5598, Ap
29	32	42.1	221	6	US-10-953-349-5597	_	5597, Ap
30	32	42.1	226	6	US-10-953-349-4194	-	4194, Ap
31	32	42.1	240	6	US-10-953-349-5596		5596, Ap
32	32	42.1	328	6	US-10-953-349-24057	Sequence	24057, A
33	32	42.1	358	6	US-10-953-349-17279	Sequence	17279, A
34	32	42.1	363	6	US-10-953-349-31909	Sequence	31909, A
35	32	42.1	366	6	US-10-953-349-17278	Sequence	17278, A
36	32	42.1	366	6	US-10-953-349-31908	-	31908, A
37	32	42.1	368	6	US-10-953-349-31907	-	31907, A
38	32	42.1	375	6	US-10-953-349-24056	_	24056, A
39	32	42.1	377	6	US-10-953-349-17277	-	17277, A
40	32	42.1	429	6	US-10-953-349-24055	-	24055, A
41	32	42.1	563	7	US-11-238-282-33		
							33, Appl
42	32	42.1	682	6	US-10-953-349-11676	-	11676, A
43	32	42.1	1018	7	US-11-293-697-2998	•	2998, Ap
44	31.5	41.4	604	6	US-10-953-349-7849	_	7849, Ap
45	31.5	41.4	623	6	US-10-953-349-7848	_	7848, Ap
46	31.5	41.4	675	6	US-10-953-349-7847	-	7847, Ap
47	31	40.8	150	6	US-10-953-349-27238	•	27238, A
48	31	40.8	209	6	US-10-953-349-11931	Sequence	11931, A
49	31	40.8	210	6	US-10-953-349-11930	Sequence	11930, A
50	31	40.8	246	6	US-10-953-349-17768	Sequence	17768, A
51	31	40.8	247	6	US-10-953-349-17767	Sequence	17767, A
52	31	40.8	255	7	US-11-293-697-4175	-	4175, Ap
53	31	40.8	302	6	US-10-953-349-7938	_	7938, Ap
54	31	40.8	311	6	US-10-953-349-7937	_	7937, Ap
55	31	40.8	326	6	US-10-953-349-7936		7936, Ap
						_	_
56	31	40.8	340	7	US-11-271-287-34		34, Appl
57	31	40.8	362	6	US-10-511-937-2608		2608, Ap
58	31	40.8	371	6	US-10-953-349-5963		5963, Ap
59	31	40.8	372	6	US-10-953-349-5962		5962, Ap
60	31	40.8	374	6	US-10-953-349-5961	_	5961, Ap
61	31	40.8	441	6	US-10-953-349-31759	-	31759, A
62	31	40.8	452	6	US-10-953-349-34342	_	34342, A
63	31	40.8	504	6	US-10-953-349-3846	Sequence	3846, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-18.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:08:52; Search time 12.1854 Seconds

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-18

Perfect score: 80

Sequence: 1 QAYEVLSDAKKRELYD 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents AA:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1 2	80 80	100.0	102 127	_	US-09-513-999C-5137 US-09-370-838-199	Sequence 5137, Ap Sequence 199, App

3	80	100.0	127	2	US-09-854-133-199	Sequence 199, App
4	80	100.0	397	1	US-08-868-288A-5	Sequence 5, Appli
5	80	100.0	397	2	US-09-235-373-5	Sequence 5, Appli
6	80	100.0	397	2	US-09-388-993-5	Sequence 5, Appli
7	80	100.0	397	2	US-09-919-039-178	Sequence 178, App
8	80	100.0	397	2	US-09-538-092-1052	Sequence 1052, Ap
	80			2	US-09-501-714-5	
9		100.0	397			Sequence 5, Appli
10	72	90.0	330	1	US-08-868-288A-3	Sequence 3, Appli
11	72	90.0	330	2	US-09-235-373-3	Sequence 3, Appli
12	72	90.0	330	2	US-09-388-993-3	Sequence 3, Appli
13	72	90.0	330	2	US-09-501-714-3	Sequence 3, Appli
14	70	87.5	334	3	US-10-429-223-3	Sequence 3, Appli
15	70	87.5	337	2	US-09-665-479A-8	Sequence 8, Appli
16	70	87.5	397	3	US-10-429-223-2	Sequence 2, Appli
				_		
17	70	87.5	397	3	US-10-429-223-4	Sequence 4, Appli
18	69	86.2	419	1	US-08-686-417-3	Sequence 3, Appli
19	64	80.0	152	2	US-09-270-767-46278	Sequence 46278, A
20	64	80.0	277	1	US-08-868-288A-7	Sequence 7, Appli
21	64	80.0	277	2	US-09-235-373-7	Sequence 7, Appli
22	64	80.0	277	2	US-09-388-993-7	Sequence 7, Appli
23	64	80.0	277	2	US-09-501-714-7	Sequence 7, Appli
24	64	80.0	327	2	US-09-949-016-11262	Sequence 11262, A
						-
25	64	80.0	351	1	US-08-868-288A-6	Sequence 6, Appli
26	64	80.0	351	2	US-09-235-373-6	Sequence 6, Appli
27	64	80.0	351	2	US-09-388-993-6	Sequence 6, Appli
28	64	80.0	351	2	US-09-501-714-6	Sequence 6, Appli
29	62	77.5	348	1	US-08-974-546-1	Sequence 1, Appli
30	62	77.5	375	2	US-09-328-352-4984	Sequence 4984, Ap
31	62	77.5	397	2	US-09-248-796A-17628	Sequence 17628, A
32	61	76.2	75	2	US-09-513-999C-6016	Sequence 6016, Ap
33	61	76.2	381	2	US-09-252-991A-27174	Sequence 27174, A
34	60	75.0	51	1	US-08-346-849-12	Sequence 12, Appl
35	60	75.0	51	1	US-08-293-284A-12	Sequence 12, Appl
36	60	75.0	51	2	US-08-898-300-12	Sequence 12, Appl
37	60	75.0	51	2	US-08-824-513-12	Sequence 12, Appl
38	60	75.0	340	1	US-08-974-546-5	Sequence 5, Appli
39	60	75.0	340	2	US-09-949-016-6691	Sequence 6691, Ap
40	60	75.0	363	2	US-09-949-016-8899	Sequence 8899, Ap
41	60	75.0	391	2	US-09-902-540-11110	Sequence 11110, A
42	59	73.8	392	2	US-09-198-452A-48	-
						Sequence 48, Appl
43	59	73.8	406	2	US-09-438-185A-34	Sequence 34, Appl
44	58	72.5	49	1	US-08-346-849-11	Sequence 11, Appl
45	58	72.5	49	1	US-08-293-284A-11	Sequence 11, Appl
46	58	72.5	49	2	US-08-898-300-11	Sequence 11, Appl
47	58	72.5	49	2	US-08-824-513-11	Sequence 11, Appl
48	58	72.5	286	2	US-09-248-796A-16992	Sequence 16992, A
49	58	72.5	358	1	US-08-868-288A-1	Sequence 1, Appli
50	58	72.5	358	2	US-09-235-373-1	Sequence 1, Appli
		72.5				Sequence 1, Appli
51	58		358	2	US-09-388-993-1	
52	58	72.5	358	2	US-09-991-181-148	Sequence 148, App
53	58	72.5	358	2	US-09-501-714-1	Sequence 1, Appli
54	58	72.5	358	2	US-09-990-444-148	Sequence 148, App
55	58	72.5	358	2	US-09-997-333-148	Sequence 148, App
56	58	72.5	358	2	US-09-992-598-148	Sequence 148, App
57	58	72.5	358	2	US-09-989-735-148	Sequence 148, App
58	58	72.5	358	3	US-09-989-726-148	Sequence 148, App
59	58	72.5	358	3	US-09-997-514-148	Sequence 148, App
60	58	72.5	358	3	US-09-989-728-148	Sequence 148, App
61	58	72.5	358	3	US-09-997-349-148	Sequence 148, App
62	58	72.5	358	3	US-09-997-653-148	Sequence 148, App
63	58	72.5	358	3	US-09-989-293A-148	Sequence 148, App

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 18.rapbm.

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OM protein - protein search, using sw model

June 2, 2006, 19:29:53; Search time 81.0596 Seconds Run on:

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-18

Perfect score: 80

Sequence: 1 QAYEVLSDAKKRELYD 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2097797 segs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA_Main:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용 Result Query No. Score Match Length DB ID Description _____ 80 100.0 16 4 US-10-001-938-18 Sequence 18, Appl

_				_		_	
2	80	100.0	127	3	US-09-738-973-199	_	199, App
3	80	100.0	127	3	US-09-854-133-199	Sequence	199, App
4	80	100.0	127	4	US-10-144-649A-199	Sequence	199, App
5	80	100.0	252	4	US-10-264-049-4191	Sequence	4191, Ap
6	80	100.0	397	3	US-09-919-039-178		178, App
7	80	100.0	397	5	US-10-473-127-1138	-	1138, Ap
8	80	100.0	397	5			
					US-10-473-127-1139	Sequence	
9	80	100.0	397	5	US-10-473-127-1140	_	1140, Ap
10	80	100.0	397	5	US-10-473-127-1143	Sequence	1143, Ap
11	80	100.0	397	5	US-10-473-127-1144	Sequence	1144, Ap
12	80	100.0	397	5	US-10-473-127-1145	Sequence	1145, Ap
13	80	100.0	397	5	US-10-756-149-4727	-	4727, Ap
14	80	100.0	397	5	US-10-631-467-559		559, App
15							
	80	100.0	397	5	US-10-878-556A-155	_	155, App
16	80	100.0	408	5	US-10-450-763-40099	-	40099, A
17	74	92.5	397	5	US-10-631-467-1386	Sequence	1386, Ap
18	73	91.2	105	4	US-10-425-115-295507	Sequence	295507,
19	72	90.0	242	4	US-10-264-049-2674	Sequence	2674, Ap
20	70	87.5	334	4	US-10-429-223-3	Sequence	-
21	70	87.5	337	4	US-10-788-792-162		162, App
22	70	87.5	397	-		_	
				4	US-10-429-223-2	Sequence	
23	70	87.5	397	4	US-10-429-223-4	Sequence	
24	69	86.2	59	4	US-10-425-115-337846	Sequence	337846,
25	69	86.2	103	4	US-10-425-115-205457	Sequence	205457,
26	69	86.2	153	4	US-10-425-115-295502	Sequence	295502,
27	69	86.2	167	4	US-10-767-701-39847	_	39847, A
28	69	86.2	183	4	US-10-425-115-295514	Sequence	
29	69	86.2	192	4	US-10-425-115-295500	_	
				-		Sequence	
30	69	86.2	194	4	US-10-425-115-295516	Sequence	
31	69	86.2	211	4	US-10-767-701-47401	Sequence	47401, A
32	69	86.2	212	4	US-10-425-115-309309	Sequence	309309,
33	69	86.2	217	4	US-10-424-599-271036	Sequence	271036,
34	69	86.2	232	5	US-10-480-988-22	Sequence	22, Appl
35	69	86.2	267	3	US-09-764-868-1164	Sequence	
36	69	86.2	267	3	US-09-764-891-4089	Sequence	_
37	69	86.2	363	4	US-10-425-115-304214	_	_
				-		Sequence	
38	69	86.2	397	4	US-10-108-260A-3837	Sequence	
39	69	86.2	410	4	US-10-424-599-271035	Sequence	•
40	69	86.2	417	4	US-10-424-599-186616	Sequence	186616,
41	69	86.2	417	4	US-10-424-599-271037	Sequence	271037,
42	69	86.2	417	4	US-10-437-963-194306	Sequence	194306,
43	69	86.2	417	4	US-10-425-115-307680	Sequence	
44	69	86.2	418	4	US-10-425-115-307678	Sequence	
45	69	86.2	418	4	US-10-425-115-307679	Sequence	
				_		-	•
46	69	86.2	419	4	US-10-437-963-194308	Sequence	
47	69	86.2	419	4	US-10-767-701-47403	-	47403, A
48	69	86.2	419	4	US-10-425-115-266771	Sequence	266771,
49	69	86.2	419	4	US-10-425-115-266773	Sequence	266773,
50	69	86.2	419	4	US-10-425-115-266781	Sequence	266781,
51	69	86.2	419	4	US-10-425-115-305086	Sequence	
52	69	86.2	419	6	US-11-096-568A-21864	_	21864, A
53	69	86.2	420	4	US-10-425-115-266776	Sequence	
54	69					_	
		86.2	421	4	US-10-425-114-63525	-	63525, A
55	69	86.2	426	4	US-10-108-260A-4751		4751, Ap
56	69	86.2	433	4	US-10-425-114-60908	Sequence	60908, A
57	69	86.2	449	4	US-10-425-114-62758	Sequence	62758, A
58	69	86.2	449	4	US-10-425-114-63503	Seguence	63503, A
59	69	86.2	449	4	US-10-425-114-65975		65975, A
60	69	86.2	449	4	US-10-425-114-73027		73027, A
61	69	86.2	450	4	US-10-425-114-46482		46482, A
62	69	86.2	450	4			
02	03	00.2	400	7	US-10-425-114-51073	sequence	51073, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-18.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:30:30; Search time 3.81457 Seconds

(without alignments)

48.509 Million cell updates/sec

Title: US-10-001-938-18

Perfect score: 80

1 QAYEVLSDAKKRELYD 16 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

> 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	80	100.0	16	6	US-10-490-949-27	Sequence 27, Appl
2	69	86.2	397	7	US-11-293-697-3837	Sequence 3837, Ap
3	69	86.2	417	6	US-10-953-349-16377	Sequence 16377, A
4	69	86.2	419	6	US-10-953-349-1054	Sequence 1054, Ap
5	69	86.2	426	7	US-11-293-697-4751	Sequence 4751, Ap
6	66	82.5	156	6	US-10-953-349-28215	Sequence 28215, A
7	66	82.5	190	6	US-10-953-349-28214	Sequence 28214, A
8	66	82.5	191	6	US-10-953-349-28213	Sequence 28213, A
9	65	81.2	382	6	US-10-953-349-13710	Sequence 13710, A
10	65	81.2	420	6	US-10-953-349-13709	Sequence 13709, A
11	64	80.0	16	6	US-10-490-949-28	Sequence 28, Appl
12	62	77.5	308	6	US-10-953-349-33811	Sequence 33811, A
13	62	77.5	336	6	US-10-953-349-33810	Sequence 33810, A
14	62	77.5	430	6	US-10-953-349-33809	Sequence 33809, A
15 16	59 59	73.8 73.8	332 367	6 6	US-10-953-349-1407	Sequence 1407, Ap
17	59 59	73.8	456	6	US-10-953-349-1406 US-10-953-349-1405	Sequence 1406, Ap
18	57	71.2	321	6	US-10-953-349-1405	Sequence 1405, Ap
19	57	71.2	323	6	US-10-953-349-949	Sequence 950, App Sequence 949, App
20	57	71.2	349	6	US-10-953-349-948	Sequence 948, App
21	5 <i>7</i>	71.2	380	6	US-10-953-349-7175	Sequence 7175, Ap
22	57	71.2	391	6	US-10-953-349-7174	Sequence 7174, Ap
23	57	71.2	442	6	US-10-953-349-7173	Sequence 7173, Ap
24	54	67.5	189	7	US-11-293-697-4556	Sequence 4556, Ap
25	54	67.5	389	7	US-11-122-986-185	Sequence 185, App
26	54	67.5	389	7	US-11-122-986-187	Sequence 187, App
27	54	67.5	583	6	US-10-953-349-35418	Sequence 35418, A
28	54	67.5	630	6	US-10-953-349-35417	Sequence 35417, A
29	53	66.2	307	6	US-10-953-349-2183	Sequence 2183, Ap
30	53	66.2	335	6	US-10-953-349-2182	Sequence 2182, Ap
31	53	66.2	343	6	US-10-953-349-2181	Sequence 2181, Ap
32	52	65.0	60	6	US-10-953-349-31081	Sequence 31081, A
33	52	65.0	95	6	US-10-953-349-31080	Sequence 31080, A
34	52	65.0	119	6	US-10-953-349-5019	Sequence 5019, Ap
35	52	65.0	119	6	US-10-953-349-28161	Sequence 28161, A
36	52	65.0	147	6	US-10-953-349-28160	Sequence 28160, A
37	52	65.0	155	6	US-10-953-349-28159	Sequence 28159, A
38	52	65.0	156	6	US-10-953-349-5018	Sequence 5018, Ap
39	52	65.0	530	6	US-10-953-349-20585	Sequence 20585, A
40	51 51	63.7 63.7	339	6	US-10-953-349-12422	Sequence 12422, A Sequence 11645, A
41 42	51 51	63.7	379	6 6	US-10-953-349-11645 US-10-953-349-32244	Sequence 32244, A
43	51	63.7	468 486	6	US-10-953-349-32244 US-10-953-349-32243	Sequence 32243, A
44	50	62.5	391	6	US-10-953-349-7627	Sequence 7627, Ap
45	49	61.3	340	6	US-10-953-349-24393	Sequence 24393, A
46	49	61.3	427	6	US-10-953-349-24392	Sequence 24392, A
47	49	61.3	445	6	US-10-953-349-24391	Sequence 24391, A
48	47	58.8	305	6	US-10-953-349-23847	Sequence 23847, A
49	45	56.2	260	7	US-11-293-697-2489	Sequence 2489, Ap
50	44	55.0	160	6	US-10-953-349-6860	Sequence 6860, Ap
51	44	55.0	199	6	US-10-953-349-9116	Sequence 9116, Ap
52	44	55.0	248	6	US-10-953-349-9115	Sequence 9115, Ap
53	43	53.8	161	6	US-10-953-349-37092	Sequence 37092, A
54	43	53.8	190	6	US-10-953-349-37091	Sequence 37091, A
55	42	52.5	138	6	US-10-953-349-20728	Sequence 20728, A
56	42	52.5	158	6	US-10-953-349-20727	Sequence 20727, A
57	42	52.5	159	6	US-10-953-349-20726	Sequence 20726, A
58	42	52.5	169	6	US-10-953-349-27713	Sequence 27713, A
59	42	52.5	465	6	US-10-953-349-8070	Sequence 8070, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-2.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 2.rai.

start

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:08:52; Search time 11.4238 Seconds

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-2

Perfect score: 82

Sequence: 1 RKAYKRLAMKYHPDR 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length :	DB	ID	Description
1		100.0		_	US-08-346-849-8	Sequence 8, Appli
2	82	100.0	52	1	US-08-293-284A-8	Sequence 8, Appli

2	0.2	100 0	E 2	2	110 00 000 200 0	Commune O Dumli
3	82	100.0	52	2	US-08-898-300-8	Sequence 8, Appli
4	82	100.0	52	2	US-08-824-513-8	Sequence 8, Appli
5	82	100.0	131	2	US-09-553-498-4	Sequence 4, Appli
6	82	100.0	131	2	US-09-618-869-4	Sequence 4, Appli
7	82	100.0	399	2	US-09-553-498-2	Sequence 2, Appli
8	82	100.0	399	2	US-09-618-869-2	Sequence 2, Appli
9	79	96.3	380	2	US-09-489-039A-9011	Sequence 9011, Ap
10	76	92.7	380	2	US-09-543-681A-5912	Sequence 5912, Ap
11	76	92.7	381	2	US-09-252-991A-27174	Sequence 27174, A
12	73	89.0	375	2	US-09-328-352-4984	
						Sequence 4984, Ap
13	68	82.9	376	3	US-10-375-010-22	Sequence 22, Appl
14	67	81.7	87	2	US-09-882-835-4	Sequence 4, Appli
15	67	81.7	102	2	US-09-513-999C-5137	Sequence 5137, Ap
16	67	81.7	127	2	US-09-370-838-199	Sequence 199, App
17	67	81.7	127	2	US-09-854-133-199	Sequence 199, App
18	67	81.7	397	1	US-08-868-288A-5	Sequence 5, Appli
19	67	81.7	397	2	US-09-235-373-5	Sequence 5, Appli
20	67	81.7	397	2	US-09-388-993-5	Sequence 5, Appli
21	67	81.7	397	2	US-09-919-039-178	Sequence 178, App
22	67	81.7	397	2	US-09-538-092-1052	Sequence 1052, Ap
23	67	81.7	397	2	US-09-501-714-5	Sequence 5, Appli
24	67	81.7	397	3	US-10-429-223-2	
25	67	81.7	397	3	US-10-429-223-2	Sequence 2, Appli
26				2		Sequence 4, Appli
	67	81.7	407		US-09-540-236-2899	Sequence 2899, Ap
27	66	80.5	392	2	US-09-198-452A-48	Sequence 48, Appl
28	66	80.5	406	2	US-09-438-185A-34	Sequence 34, Appl
29	65	79.3	348	1	US-08-974-546-1	Sequence 1, Appli
30	63	76.8	52	1	US-08-346-849-10	Sequence 10, Appl
31	63	76.8	52	1	US-08-293-284A-10	Sequence 10, Appl
32	63	76.8	52	2	US-08-898-300-10	Sequence 10, Appl
33	63	76.8	52	2	US-08-824-513-10	Sequence 10, Appl
34	63	76.8	96	2	US-09-621-976-4045	Sequence 4045, Ap
35	63	76.8	147	2	US-09-270-767-33311	Sequence 33311, A
36	63	76.8	147	2	US-09-270-767-48528	Sequence 48528, A
37	63	76.8	147	2	US-09-513-999C-6925	Sequence 6925, Ap
38	63	76.8	223	2	US-09-658-644-4	Sequence 4, Appli
39	63	76.8	223	2	US-09-949-016-6832	Sequence 6832, Ap
40	63	76.8	267	2	US-09-949-016-11497	Sequence 11497, A
41	62	75.6	51	1	US-08-346-849-12	Sequence 12, Appl
42	62	75.6	51	1	US-08-293-284A-12	
						Sequence 12, Appl
43	62	75.6	51			Sequence 12, Appl
44	62	75.6	51	2	US-08-824-513-12	Sequence 12, Appl
45	62	75.6	199	2	US-09-248-796A-16959	Sequence 16959, A
46	62	75.6	206	2	US-09-830-230A-294	Sequence 294, App
47	62	75.6	250	2	US-09-830-230A-293	Sequence 293, App
48	62	75.6	320	2	US-09-328-352-7937	Sequence 7937, Ap
49	62	75.6	330	1	US-08-868-288A-3	Sequence 3, Appli
50	62	75.6	330	2	US-09-235-373-3	Sequence 3, Appli
51	62	75.6	330	2	US-09-388-993-3	Sequence 3, Appli
52	62	75.6	330	2	US-09-501-714-3	Sequence 3, Appli
53	62	75.6	347	2	US-09-248-796A-19195	Sequence 19195, A
54	62	75.6	382	2	US-09-603-208A-40	Sequence 40, Appl
55	62	75.6	391	2	US-09-902-540-11110	Sequence 11110, A
56	62	75.6	397	2	US-09-248-796A-17628	Sequence 17628, A
57	61	74.4	185	2	US-09-134-000C-6695	Sequence 6695, Ap
58	61	74.4	734	2	US-09-134-000C-8693	-
59	60		75	2		Sequence 16776, A
		73.2			US-09-513-999C-6016	Sequence 6016, Ap
60	59 50	72.0	54	1	US-08-346-849-13	Sequence 13, Appl
61	59 50	72.0	54	1	US-08-293-284A-13	Sequence 13, Appl
62	59 50	72.0	54	2	US-08-898-300-13	Sequence 13, Appl
63	59	72.0	54	2	US-08-824-513-13	Sequence 13, Appl

SCORE Search Results Details for Application 100 and Search Result us-10-001-938-2.rapbm

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start

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OM protein - protein search, using sw model

June 2, 2006, 19:29:53; Search time 75.9934 Seconds Run on:

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-2

Perfect score: 82

Sequence: 1 RKAYKRLAMKYHPDR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

2097797 segs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA Main:* Database :

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	82	100.0	15	4	US-10-001-938-2	Sequence 2, Appli
2	82	100.0	52	4	US-10-390-472-8	Sequence 8, Appli
3	82	100.0	376	4	US-10-369-493-689	Sequence 689, App

				_			
4	82	100.0	376	6	US-11-080-458-32	Sequence	32, Appl
5	82	100.0	476	5	US-10-450-763-48130	Sequence	48130, A
6	79	96.3	378	4	US-10-369-493-21305	Sequence	21305, A
7	75	91.5	378	4	US-10-369-493-386	Seguence	386, App
8	73	89.0	158	4	US-10-425-114-48912	-	48912, A
9	73	89.0	326	4	US-10-425-115-300448	Sequence	
10	73	89.0	369	4	US-10-369-493-19646		19646, A
				_		_	
11	71	86.6	362	4	US-10-369-493-9305	-	9305, Ap
12	71	86.6	374	4	US-10-369-493-13658	-	13658, A
13	71	86.6	375	4	US-10-369-493-15859	-	15859, A
14	71	86.6	376	4	US-10-369-493-15487	Sequence	15487, A
15	70	85.4	230	5	US-10-467-657-3888	Sequence	3888, Ap
16	69	84.1	276	4	US-10-282-122A-47226	Sequence	47226, A
17	68	82.9	42	4	US-10-437-963-128035	Sequence	128035,
18	68	82.9	153	4	US-10-424-599-257493	Sequence	
19	68	82.9	166	4	US-10-437-963-119078	Sequence	
20	68	82.9	166	4	US-10-425-115-238005	Sequence	
21	68	82.9	168	4	US-10-425-115-252651	Sequence	
22	68	82.9	217	4	US-10-423-113-232031 US-10-424-599-257471	-	•
				_		Sequence	
23	68	82.9	248	4	US-10-424-599-191917	Sequence	
24	68	82.9	276	4	US-10-424-599-191915	Sequence	
25	68	82.9	276	6	US-11-096-568A-8289	-	8289, Ap
26	68	82.9	289	4	US-10-424-599-192793	Sequence	
27	68	82.9	306	6	US-11-039-722-4	Sequence	4, Appli
28	68	82.9	376	4	US-10-375-010-22	Sequence	22, Appl
29	68	82.9	376	6	US-11-232-406A-22	Sequence	22, Appl
30	68	82.9	378	4	US-10-369-493-8450	Sequence	8450, Ap
31	68	82.9	379	4	US-10-369-493-7330	_	7330, Ap
32	68	82.9	380	4	US-10-369-493-4573	-	4573, Ap
33	67	81.7	15	4	US-10-001-938-14	_	14, Appl
34	67	81.7	58	4	US-10-335-977-7661	_	7661, Ap
35	67	81.7	66	6	US-11-039-722-7	_	7, Appli
36	67	81.7	69	4	US-10-335-977-7663		7663, Ap
37	67	81.7	87	4	US-10-135-577-7665	-	_
				-			48, Appl
38	67	81.7	127	3	US-09-738-973-199		199, App
39	67 67	.81.7	127	3	US-09-854-133-199		199, App
40	67	81.7	127	4	US-10-144-649A-199		199, App
41	67	81.7	150	4	US-10-425-115-206200	Sequence	
42	67	81.7	154	4	US-10-424-599-217994	Sequence	
43	67	81.7	334	4	US-10-161-051-134		134, App
44	67	81.7	334	6	US-11-097-143-22242	Sequence	22242, A
45	67	81.7	369	3	US-09-895-913A-180	Sequence	180, App
46	67	81.7	369	4	US-10-335-977-7666	Sequence	7666, Ap
47	67	81.7	379	4	US-10-369-493-22783	Sequence	22783, A
48	67	81.7	397	3	US-09-919-039-178	Sequence	178, App
49	67	81.7	397	4	US-10-108-260A-3837	_	3837, Ap
50	67	81.7	397	4	US-10-429-223-2		2, Appli
51	67	81.7	397	4	US-10-429-223-4		4, Appli
52	67	81.7	397	5	US-10-473-127-1138		1138, Ap
53	67	81.7	397	5	US-10-473-127-1139		1139, Ap
54	67	81.7	397	5	US-10-473-127-1140	_	1140, Ap
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56	67	81.7	397	5	US-10-473-127-1144		1144, Ap
57	67	81.7	397	5	US-10-473-127-1145		1145, Ap
58	67	81.7	397	5	US-10-756-149-4727		4727, Ap
59	67	81.7	397	5	US-10-631-467-559		559, App
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61	67	81.7	397	5	US-10-878-556A-155		155, App
62	67	81.7	403	6	US-11-097-143-24405		24405, A
63	67	81.7	403	6	US-11-097-143-41904		41904, A
64	67	81.7	408	5	US-10-450-763-40099	Sequence	40099, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-2.rapbn.

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SCORE FAQ

Comments / Suggestions

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-2.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

US-10-001-938-2 Title:

Perfect score: 82

1 RKAYKRLAMKYHPDR 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

> 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

> 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	82	100.0	15	6	US-10-490-949-3	Sequence 3, Appli
2	67	81.7	15	6	US-10-490-949-23	Sequence 23, Appl
3	67	81.7	397	7	US-11-293-697-3837	Sequence 3837, Ap
4	65	79.3	95	6	US-10-953-349-31080	Sequence 31080, A
5	65	79.3	156	6	US-10-953-349-5018	Sequence 5018, Ap
6	65	79.3	335	6	US-10-953-349-2182	Sequence 2182, Ap
7	65	79.3	343	6	US-10-953-349-2181	Sequence 2181, Ap
8	63	76.8	349	6	US-10-953-349-948	Sequence 948, App
9	62	75.6	336	6	US-10-953-349-33810	Sequence 33810, A
10	62	75.6	430	6	US-10-953-349-33809	Sequence 33809, A
11	61	74.4	465	6	US-10-953-349-8070	Sequence 8070, Ap
12	61	74.4	473	6	US-10-953-349-8069	Sequence 8069, Ap
13	61	74.4	482	6	US-10-953-349-8068	Sequence 8068, Ap
14	60	73.2	305	6	US-10-953-349-23847	Sequence 23847, A
15	59	72.0	190	6	US-10-953-349-28214	Sequence 28214, A
16	59	72.0	191	6	US-10-953-349-28213	Sequence 28213, A
17	59	72.0	199	6	US-10-953-349-9116	Sequence 9116, Ap
18	59	72.0	248	6	US-10-953-349-9115	Sequence 9115, Ap
19	59	72.0	273	6	US-10-953-349-4464	Sequence 4464, Ap
20	59	72.0	349	6	US-10-953-349-4463	Sequence 4463, Ap
21	59	72.0	367	6	US-10-953-349-4462	Sequence 4462, Ap
22	59	72.0	389	7	US-11-122-986-185	Sequence 185, App
23	59	72.0	389	7	US-11-122-986-187	Sequence 187, App
24	58	70.7	15	6	US-10-490-949-22	Sequence 22, Appl
25	58	70.7	426	7	US-11-293-697-4751	Sequence 4751, Ap
26	56	68.3	313	6	US-10-953-349-23774	Sequence 23774, A
27	56	68.3	334	6	US-10-953-349-23773	Sequence 23773, A
28	56	68.3	420	6	US-10-953-349-13709	Sequence 13709, A
29	56	68.3	583	6	US-10-953-349-35418	Sequence 35418, A
30	56	68.3	605	6	US-10-953-349-2076	Sequence 2076, Ap
31 32	56 56	68.3 68.3	619 630	6 6	US-10-953-349-2075 US-10-953-349-2074	Sequence 2075, Ap
33	56	68.3	630	6	US-10-953-349-2074 US-10-953-349-35417	Sequence 2074, Ap Sequence 35417, A
34	55	67.1	15	6	US-10-933-349-33417	Sequence 21, Appl
35	55	67.1	338	6	US-10-953-349-20361	Sequence 20361, A
36	55	67.1	385	6	US-10-953-349-20360	Sequence 20360, A
37	55	67.1	417	6	US-10-953-349-16377	Sequence 16377, A
38	55	67.1	419	6	US-10-953-349-1054	Sequence 1054, Ap
39	55	67.1	488	6	US-10-953-349-20359	Sequence 20359, A
40	54	65.9	504	6	US-10-511-937-2547	Sequence 2547, Ap
41	53	64.6	110	6	US-10-953-349-54	Sequence 54, Appl
42	53	64.6	124	6	US-10-953-349-53	Sequence 53, Appl
43	53	64.6	162	6	US-10-953-349-52	Sequence 52, Appl
44	53	64.6	530	6	US-10-953-349-20585	Sequence 20585, A
45	52	63.4	380	6	US-10-953-349-7175	Sequence 7175, Ap
46	52	63.4	391	6	US-10-953-349-7174	Sequence 7174, Ap
47	52	63.4	442	6	US-10-953-349-7173	Sequence 7173, Ap
48	51	62.2	333	6	US-10-953-349-2863	Sequence 2863, Ap
49	51	62.2	333	6	US-10-953-349-11247	Sequence 11247, A
50	46	56.1	119	6	US-10-953-349-28161	Sequence 28161, A
51	46	56.1	138	6	US-10-953-349-39107	Sequence 39107, A
52	46	56.1	147	6	US-10-953-349-28160	Sequence 28160, A
53	46	56.1	155	6	US-10-953-349-28159	Sequence 28159, A
54	46	56.1	157	6	US-10-953-349-38105	Sequence 38105, A
55	46	56.1	174	6	US-10-953-349-39106	Sequence 39106, A
56	46	56.1	189	7	US-11-293-697-4556	Sequence 4556, Ap
57	46	56.1	192	6	US-10-953-349-38104	Sequence 38104, A
58	46	56.1	367	6	US-10-953-349-1406	Sequence 1406, Ap
59	46	56.1	456	6	US-10-953-349-1405	Sequence 1405, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-20

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 20.rai.

start

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:12:07; Search time 12.7 Seconds (without alignments)

102 303 Million cell undates/sec

103.383 Million cell updates/sec

Title: US-10-001-938-20

Perfect score: 83

Sequence: 1 SGPFFTFSSSFPGHS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	277	1	US-08-868-288A-7	Sequence 7, Appli
2	83		277	2	US-09-235-373-7	Sequence 7, Appli

3	83	100.0	277	2	US-09-388-993-7	Sequence	
4	83	100.0	277	2	US-09-501-714-7	Sequence	7, Appli
5	83	100.0	327	2	US-09-949-016-11262	Sequence	11262, A
6	83	100.0	351	1	US-08-868-288A-6	Sequence	6, Appli
7	83	100.0	351	2	US-09-235-373-6	Sequence	6, Appli
8	83	100.0	351	2	US-09-388-993-6	Sequence	6, Appli
9	83	100.0	351	2	US-09-501-714-6	_	6, Appli
10	46	55.4	661	2	US-09-949-016-9121	Sequence	
11	40	48.2	190	2	US-09-270-767-58877		58877, A
			201	1	US-08-155-171B-19	Sequence	
12	40	48.2				-	
13	40	48.2	201	1	US-08-435-998-19	Sequence	
14	40	48.2	204	1	US-08-155-171B-20	Sequence	
15	40	48.2	204	1	US-08-435-998-20		20, Appl
16	40	48.2	205	1	US-08-155-171B-17	Sequence	
17	40	48.2	205	1	US-08-435-998-17	Sequence	17, Appl
18	40	48.2	206	1	US-08-155-171B-6	Sequence	6, Appli
19	40	48.2	206	1	US-08-435-998-6	Sequence	6, Appli
20	40	48.2	209	1	US-08-155-171B-18	Sequence	18, Appl
21	40	48.2	209	1	US-08-435-998-18	Sequence	18, Appl
22	40	48.2	238	2	US-09-949-016-6334		6334, Ap
23	40	48.2	255	2	US-09-949-016-9861	-	9861, Ap
24	40	48.2	280	1	US-08-855-140-1		1, Appli
			286		US-09-270-767-43514		43514, A
25	40	48.2		2			
26	40	48.2	297	2	US-10-104-047-2852	_	2852, Ap
27	40	48.2	371	2	US-09-828-302-15	_	15, Appl
28	40	48.2	481	2	US-09-949-016-9509		9509, Ap
29	40	48.2	1066	1	US-08-633-770A-1		1, Appli
30	40	48.2	1066	2	US-09-280-197-5	Sequence	5, Appli
31	40	48.2	1066	2	US-09-423-126-3	Sequence	3, Appli
32	39	47.0	192	2	US-09-252-991A-32913	Sequence	32913, A
33	39	47.0	236	2	US-08-705-771-19	Sequence	19, Appl
34	39	47.0	236	2	US-09-417-540-19	Sequence	19, Appl
35	39	47.0	259	2	US-09-585-645A-66		66, Appl
36	39	47.0	265	1	US-08-807-044-1	-	1, Appli
37	39	47.0	513	2	US-09-862-631-4		4, Appli
38	39	47.0	529	2	US-09-801-042-2		2, Appli
39	39	47.0	565	2	US-09-489-039A-13730		13730, A
40	39	47.0	578	2	US-09-252-991A-16850		16850, A
				2			
	38.5	46.4	448		US-09-198-452A-216	-	216, App
42	38.5	46.4	457	2	US-09-438-185A-199		199, App
43	38	45.8	88	2	US-09-513-999C-7631	-	7631, Ap
44	38	45.8	150	2	US-09-540-236-3000		3000, Ap
45	38	45.8	319	2	US-09-248-796A-15068	_	15068, A
46	38	45.8	367	2	US-09-949-016-6722	_	6722, Ap
47	38	45.8	405	2	US-09-949-016-9688	Sequence	9688, Ap
48	38	45.8	512	2	US-09-489-039A-10100	Sequence	10100, A
49	38	45.8	540	2	US-10-094-749-3182	Sequence	3182, Ap
50	38	45.8	548	2	US-09-489-039A-8097	Sequence	8097, Ap
51	37	44.6	33	1	US-08-155-171B-12	Sequence	12, Appl
52	37	44.6	33	1	US-08-435-998-12		12, Appl
53	37	44.6	61	2	US-09-621-976-5856		5856, Ap
54	37	44.6	61	2	US-09-621-976-5857		5857, Ap
55	37	44.6	61	2	US-09-621-976-5872		5872, Ap
56	37	44.6	105	2	US-10-104-047-3817		3817, Ap
							10567, Ap
57	37	44.6	119	2	US-09-902-540-10567		
58	37	44.6	135	2	US-09-355-040-15		15, Appl
59	37	44.6	150	2	US-09-252-991A-24718		24718, A
60	37	44.6	203	2	US-09-248-796A-16268	_	16268, A
61	37	44.6	204	1	US-08-155-171B-2	_	2, Appli
62	37	44.6	204	1	US-08-435-998-2		2, Appli
63	37	44.6	267	2	US-09-270-767-37278	Sequence	37278, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 20.rapbm.

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<u>start</u>

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OM protein - protein search, using sw model

June 2, 2006, 19:45:16; Search time 63.4 Seconds Run on:

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-20

Perfect score: 83

Sequence: 1 SGPFFTFSSSFPGHS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

2097797 segs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용 Result Query No. Score Match Length DB ID Description 1 83 100.0 15 4 US-10-001-938-20 Sequence 20, Appl

2	50	60.2	123	3	US-09-925-297-862	Sequence	862, App
3	49	59.0	137	4	US-10-425-115-269076	Sequence	-
4	47	56.6	48	4	US-10-425-115-200603	Sequence	
5	47	56.6	268	4	US-10-282-122A-63570	•	63570, A
6	46			_			
		55.4	79	4	US-10-425-115-244806	Sequence	
7	46	55.4	625	4	US-10-072-012-699		699, App
8	46	55.4	625	5	US-10-029-345A-39		39, Appl
9	46	55.4	625	5	US-10-029-345A-110	Sequence	110, App
10	46	55.4	625	6	US-11-143-984A-39	Sequence	39, Appl
11	46	55.4	625	6	US-11-143-984A-110		110, App
12	46	55.4	663	4	US-10-072-012-700	-	700, App
13	46	55.4	663	5			
					US-10-029-345A-40	_	40, Appl
14	46	55.4	663	6	US-11-143-984A-40		40, Appl
15	45	54.2	129	5	US-10-720-603A-26	Sequence	26, Appl
16	45	54.2	283	4	US-10-437-963-199254	Sequence	199254,
17	44	53.0	115	4	US-10-424-599-152729	Sequence	152729,
18	44	53.0	302	4	US-10-425-114-53866	_	53866, A
19	44	53.0	314	4	US-10-425-115-351784	Sequence	
20	43	51.8	38	4	US-10-437-963-122150	Sequence	
				_			
21	43	51.8	53	4	US-10-767-701-62139		62139, A
22	43	51.8	93	4	US-10-425-115-317926	Sequence	
23	43	51.8	204	6	US-11-087-099-10169	Sequence	10169, A
24	43	51.8	216	4	US-10-425-114-60968	Sequence	60968, A
25	43	51.8	243	5	US-10-739-930-10203	Sequence	10203, A
26	43	51.8	261	4	US-10-425-115-262629	Sequence	
27	43	51.8	269	6	US-11-096-568A-15319	-	15319, A
28	43	51.8	283	4	US-10-437-963-126681	Sequence	
				_		_	
29	43	51.8	285	4	US-10-767-701-44420	-	44420, A
30	43	51.8	289	6	US-11-087-099-6104		6104, Ap
31	43	51.8	292	6	US-11-087-099-5026	Sequence	5026, Ap
32	43	51.8	292	6	US-11-087-099-12088	Sequence	12088, A
33	43	51.8	292	6	US-11-096-568A-15318	Sequence	15318, A
34	43	51.8	294	4	US-10-425-115-262631	Sequence	
35	43	51.8	351	6	US-11-096-568A-31831	~	31831, A
36	43	51.8	358	6	US-11-096-568A-15317		15317, A
37	43	51.8	378	6	US-11-188-298-17261	_	17261, A
38	43	51.8	395	6	US-11-096-568A-31830	_	31830, A
39	43	51.8	400	6	US-11-096-568A-31829		31829, A
40	43	51.8	400	6	US-11-242-650-50	Sequence	50, Appl
41	43	51.8	912	4	US-10-437-963-140140	Sequence	140140,
42	42	50.6	119	4	US-10-425-115-309236	Sequence	309236,
43	42	50.6	127	4	US-10-424-599-269871	Sequence	
44	42	50.6	129	4	US-10-425-115-349086	Sequence	
45	42	50.6	129	5	US-10-720-603A-31		31, Appl
46	42	50.6	145	4	US-10-425-115-276721	Sequence	
47	42	50.6	343	4	US-10-156-761-14087		14087, A
48	42	50.6	359	3	US-09-764-864-996		996, App
49	42	50.6	402	5	US-10-719-993-465	Sequence	465, App
50	42	50.6	441	5	US-10-719-993-461	Sequence	461, App
51	42	50.6	441	5	US-10-719-993-463	Sequence	463, App
52	42	50.6	590	5	US-10-719-993-462		462, App
53	42	50.6	1020	5	US-10-719-993-464		464, App
54							
	42	50.6	1229	6	US-11-097-143-42000		42000, A
55	41.5	50.0	1010	4	US-10-437-963-180288	Sequence	
56	41	49.4	44	4	US-10-424-599-221131	Sequence	
57	41	49.4	44	4	US-10-425-115-232702	Sequence	232702,
58	41	49.4	65	4	US-10-437-963-148528	Sequence	148528,
59	41	49.4	70	4	US-10-424-599-193370	Sequence	
60	41	49.4	76	4	US-10-425-115-186010	Sequence	
61	41	49.4	97	4	US-10-425-115-367760	Sequence	
62	41	49.4	102	4	US-10-425-115-367760 US-10-425-115-217338	Sequence	
02	41	32.4	102	7	05 10 425-115-21/350	Sequence	21,330,

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-20.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-20

Perfect score: 83

Sequence:

1 SGPFFTFSSSFPGHS 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters:

58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	83	100.0	15	6	US-10-490-949-29	Sequence 29, Appl
2	43	51.8	265	6	US-10-953-349-11490	Sequence 11490, A
3	43	51.8	309	6	US-10-953-349-11489	Sequence 11489, A
4	43	51.8	314	6	US-10-953-349-11488	Sequence 11488, A
5	43	51.8	400	7	US-11-266-446-50	Sequence 50, Appl
6	40	48.2	236	6	US-10-953-349-7596	Sequence 7596, Ap
7	40	48.2	266	6	US-10-953-349-7595	Sequence 7595, Ap
8 9	39 39	47.0 47.0	216 226	6 6	US-10-953-349-36980 US-10-953-349-36979	Sequence 36980, A Sequence 36979, A
10	39	47.0	425	6	US-10-953-349-2574	Sequence 2574, Ap
11	38	45.8	404	7	US-11-293-697-4601	Sequence 4601, Ap
12	37	44.6	202	7	US-11-293-697-3481	Sequence 3481, Ap
13	37	44.6	250	6	US-10-953-349-34062	Sequence 34062, A
14	37	44.6	269	6	US-10-953-349-34061	Sequence 34061, A
15	37	44.6	274	6	US-10-953-349-34060	Sequence 34060, A
16	37	44.6	437	7	US-11-293-697-3820	Sequence 3820, Ap
17	37	44.6	641	7	US-11-293-697-3240	Sequence 3240, Ap
18	37	44.6	1336	7	US-11-106-014-92	Sequence 92, Appl
19	36	43.4	192	7	US-11-264-509A-1	Sequence 1, Appli
20	36	43.4	245	6	US-10-953-349-6742	Sequence 6742, Ap
21	36	43.4	259	6	US-10-953-349-6741	Sequence 6741, Ap
22	36	43.4	263	6	US-10-953-349-18437	Sequence 18437, A
23	36	43.4	320	6	US-10-953-349-18436	Sequence 18436, A
24	36 36	43.4	321 340	6 6	US-10-953-349-12608	Sequence 12608, A
25 26	36 36	43.4 43.4	392	6	US-10-953-349-18435 US-10-953-349-12607	Sequence 18435, A Sequence 12607, A
27	36	43.4	422	6	US-10-953-349-12606	Sequence 12606, A
28	36	43.4	496	7	US-11-254-252-6	Sequence 6, Appli
29	36	43.4	635	7	US-11-254-252-14	Sequence 14, Appl
30	36	43.4	751	7	US-11-254-252-12	Sequence 12, Appl
31	36	43.4	3011	7	US-11-140-487A-771	Sequence 771, App
32	36	43.4	3011	7	US-11-236-836-14	Sequence 14, Appl
33	36	43.4	3011	7	US-11-254-252-20	Sequence 20, Appl
34	35	42.2	100	7	US-11-293-697-2621	Sequence 2621, Ap
35	35	42.2		7	US-11-293-697-4841	Sequence 4841, Ap
36	35	42.2	110	7	US-11-293-697-3004	Sequence 3004, Ap
37	35	42.2	170	6	US-10-953-349-34677	Sequence 34677, A
38	35	42.2	270	6	US-10-953-349-2099	Sequence 2099, Ap
39	35	42.2 42.2	277	6	US-10-953-349-23050 US-10-953-349-23049	Sequence 23050, A
40 41	35 35	42.2	286 315	6 6	US-10-953-349-23049 US-10-953-349-2098	Sequence 23049, A Sequence 2098, Ap
42	35	42.2	334	6	US-10-953-349-23563	Sequence 23563, A
43	35	42.2	337	6	US-10-953-349-2097	Sequence 2007, Ap
44	35	42.2	357	6	US-10-953-349-23048	Sequence 23048, A
45	35	42.2	417	6	US-10-953-349-23562	Sequence 23562, A
46	35	42.2	425	6	US-10-953-349-23561	Sequence 23561, A
47	35	42.2	471	7	US-11-293-697-4551	Sequence 4551, Ap
48	35	42.2	476	6	US-10-505-928-588	Sequence 588, App
49	34	41.0	164	6	US-10-953-349-36053	Sequence 36053, A
50	34	41.0	167		US-10-953-349-37948	Sequence 37948, A
51	34	41.0	176		US-10-953-349-31456	Sequence 31456, A
52	34	41.0	176		US-10-953-349-36052	Sequence 36052, A
53	34	41.0			US-10-953-349-37947	Sequence 37947, A
54 55	34	41.0			US-10-953-349-14070 US-10-953-349-14069	Sequence 14070, A Sequence 14069, A
56	34 34	41.0 41.0	249 256		US-10-953-349-4076	Sequence 4076, Ap
57	34	41.0	273		US-10-953-349-14068	Sequence 14068, A
58	34	41.0			US-10-505-928-847	Sequence 847, App
59	34	41.0	325		US-10-953-349-4075	Sequence 4075, Ap
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SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-21.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 21.rai.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:08:52; Search time 11.4238 Seconds

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-21

Perfect score: 78

Sequence: 1 DGQLKSVTINGVPDD 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents AA:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:* 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1 2	78 78	100.0		_	US-08-868-288A-7 US-09-235-373-7	Sequence 7, Appli Sequence 7, Appli

3	78	100.0	277	2	US-09-388-993-7		7, Appli
4	78	100.0	277	2	US-09-501-714-7	Sequence	7, Appli
5	78	100.0	327	2	US-09-949-016-11262	Sequence	11262, A
6	78	100.0	351	1	US-08-868-288A-6	-	6, Appli
7	78	100.0	351	2	US-09-235-373-6	_	6, Appli
8	78	100.0	351	2	US-09-388-993-6		6, Appli
			351	2			
9	78	100.0			US-09-501-714-6		6, Appli
10	67	85.9	330	1	US-08-868-288A-3	_	3, Appli
11	67	85.9	330	2	US-09-235-373-3		3, Appli
12	67	85.9	330	2	US-09-388-993-3		3, Appli
13	67	85.9	330	2	US-09-501-714-3	Sequence	3, Appli
14	44	56.4	1233	2	US-09-134-000C-4971	Sequence	4971, Ap
15	44	56.4	1416	2	US-09-071-035-404	Sequence	404, App
16	44	56.4	1416	2	US-10-206-576-404	Sequence	404, App
17	44	56.4	1448	2	US-09-071-035-402	-	402, App
18	44	56.4	1448	2	US-10-206-576-402	-	402, App
19	42.5	54.5	287	2	US-09-489-039A-10311	-	10311, A
20	40	51.3	333	2	US-09-270-767-46345	_	46345, A
						_	
21	40	51.3	497	1	US-09-047-125-3		3, Appli
22	40	51.3	497	2	US-07-736-335E-3	•	3, Appli
23	40	51.3	497	2	US-08-709-731A-29	_	29, Appl
24	40	51.3	544	2	US-09-902-540-15796	Sequence	15796, A
25	40	51.3	873	2	US-09-248-796A-20365	Sequence	20365, A
26	39	50.0	418	2	US-09-843-905A-2	Sequence	2, Appli
27	39	50.0	418	2	US-09-843-905A-4		4, Appli
28	39	50.0	446	2	US-09-252-991A-21834	-	21834, A
29	39	50.0	546	2	US-09-252-991A-22048		22048, A
30	39	50.0	636	2	US-09-328-352-5495		5495, Ap
	38	48.7	242	2	US-09-286-690-8		8, Appli
31						_	
32	38	48.7	306	2	US-09-270-767-59593	-	59593, A
33	38	48.7	390	1	US-08-335-583C-2		2, Appli
34	38	48.7	503	2	US-09-252-991A-18345		18345, A
35	38	48.7	568	2	US-09-248-796A-22993	_	22993, A
36	38	48.7	752	2	US-09-248-796A-15445	_	15445, A
37	38	48.7	768	2	US-09-540-236-3811	Sequence	3811, Ap
38	38	48.7	794	2	US-09-248-796A-18919	Sequence	18919, A
39	38	48.7	887	2	US-10-132-350-18	Sequence	18, Appl
40	38	48.7	887	2	US-10-132-350-20	Sequence	20, Appl
41	38	48.7	991	2	US-09-902-540-11984	Sequence	11984, A
42	38	48.7	1105	2	US-09-270-767-44167	-	44167, A
43	38	48.7	2749	2	US-10-360-101-265		265, App
44	37	47.4	221	2	US-09-710-279-2216		2216, Ap
45	37	47.4	248	2	US-10-147-874-3		3, Appli
				2	US-09-328-352-6547		6547, Ap
46	37	47.4	352				
47	37	47.4	364	2	US-09-489-039A-12541		12541, A
48	37	47.4	366	2	US-09-040-681A-6		6, Appli
49	37	47.4	366	2	US-09-497-897-6		6, Appli
50	37	47.4	392	2	US-09-013-881-2		2, Appli
51	37	47.4	392	2	US-09-612-473-2		2, Appli
52	37	47.4	392	2	US-09-724-730-2		2, Appli
53	37	47.4	396	2	US-09-252-991A-19425	Sequence	19425, A
54	37	47.4	397	2	US-09-134-001C-5504	Sequence	5504, Ap
55	37	47.4	548	2	US-09-543-681A-6631	Sequence	6631, Ap
56	37	47.4	724	2	US-09-543-681A-4745	Sequence	4745, Ap
57	37	47.4	739	2	US-09-248-796A-19328		19328, A
58	37	47.4	754	2	US-09-543-681A-5416	_	5416, Ap
59	37	47.4	975	2	US-09-540-236-2304	_	2304, Ap
60	36	46.2	67	2	US-09-540-236-2115		2115, Ap
	36	46.2	119	2	US-09-902-540-10138		10138, A
61 62			158	2	US-09-270-767-31806		31806, A
62 63	36 36	46.2		2			15490, A
63	36	46.2	197	4	US-09-248-796A-15490	Sequence	10470' W

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 21.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 21.rapbm.

start

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:29:53; Search time 75.9934 Seconds

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-21

Perfect score: 78

Sequence: 1 DGQLKSVTINGVPDD 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA Main:* Database :

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용 Result Query No. Score Match Length DB ID Description 78 100.0 15 4 US-10-001-938-21 Sequence 21, Appl

2	54	69.2	232	5	US-10-480-988-22	Sequence	22, Appl
3	54	69.2	267	3	US-09-764-868-1164	Sequence	1164, Ap
4	54	69.2	267	3	US-09-764-891-4089	Sequence	4089, Ap
5	52	66.7	242	4	US-10-264-049-2674	Sequence	2674, Ap
6	50	64.1	343	4	US-10-032-201B-274	Sequence	
7	45	57.7	589	4	US-10-260-937-36	Sequence	
8	44.5	57.1	745	6	US-11-079-463-6408		6408, Ap
9	44	56.4	509	5	US-10-732-923-23606		23606, A
10	44	56.4	968	6	US-11-097-143-20043	_	20043, A
						-	
11	44	56.4	1416	3	US-09-071-035-404	Sequence	
12	44	56.4	1416	4	US-10-206-576-404	Sequence	
13	44	56.4	1416	5	US-10-912-362-404	Sequence	
14	44	56.4	1448	3	US-09-071-035-402	Sequence	
15	44	56.4	1448	4	US-10-206-576-402		402, App
16	44	56.4	1448	5	US-10-912-362-402	Sequence	402, App
17	43	55.1	251	6	US-11-098-686-11007	Sequence	11007, A
18	42	53.8	94	4	US-10-425-115-321280	Sequence	321280,
19	42	53.8	115	4	US-10-425-115-311609	Sequence	311609,
20	42	53.8	525	4	US-10-425-114-44083	_	44083, A
21	42	53.8	620	4	US-10-408-765A-1812	-	1812, Ap
22	42	53.8	692	4	US-10-424-599-150564	Sequence	
23	42	53.8	730	4	US-10-042-865-51	-	51, Appl
						_	
24	42	53.8	730	4	US-10-029-020-50		50, Appl
25	42	53.8	730	4	US-10-408-765A-2505		2505, Ap
26	42	53.8	730	6	US-11-113-424-50	_	50, Appl
27	42	53.8	847	5	US-10-778-804-8	_	8, Appli
28	42	53.8	847	5	US-10-778-804-9		9, Appli
29	42	53.8	1086	5	US-10-723-860-3170	Sequence	3170, Ap
30	42	53.8	1086	5	US-10-756-149-5574	Sequence	5574, Ap
31	42	53.8	1688	4	US-10-144-194A-113	Sequence	113, App
32	42	53.8	1688	5	US-10-491-566-113	Sequence	113, App
33	42	53.8	1688	5	US-10-494-940-52		52, Appl
34	42	53.8	1737	3	US-09-808-602-83		83, Appl
35	42	53.8	1737	3	US-09-800-198-71		71, Appl
36	42	53.8	2144	5	US-10-723-860-2303		2303, Ap
37	42	53.8	2333	5	US-10-453-372-170	_	170, App
38	42	53.8	2551	4	US-10-144-194A-80	_	80, Appl
39	42	53.8	2551	5	US-10-144-154A-00	_	80, Appl
				4	US-10-144-194A-82		82, Appl
40	42	53.8	2633	-		_	
41	42	53.8	2633	5	US-10-491-566-82	=	82, Appl
42	42	53.8	2662	5	US-10-453-372-114	_	114, App
43	42	53.8	2724	3	US-09-808-602-13		13, Appl
44	42	53.8	2724	3	US-09-800-198-13		13, Appl
45	42	53.8	2724	5	US-10-453-372-148	_	148, App
46	42	53.8	2733	3	US-09-808-602-8	Sequence	8, Appli
47	42	53.8	2733	3	US-09-800-198-8	Sequence	8, Appli
48	42	53.8	2733	5	US-10-453-372-136	Sequence	136, App
49	42	53.8	2733	5	US-10-453-372-142	Sequence	142, App
50	42	53.8	2733	5	US-10-453-372-146		146, App
51	42	53.8	2733	5	US-10-453-372-150		150, App
52	42	53.8	2733	5	US-10-453-372-154		154, App
53	42	53.8	2758	4	US-10-467-535-10	-	10, Appl
54	42	53.8	2764	3	US-09-808-602-80		80, Appl
		53.8			US-09-800-198-68		68, Appl
55	42		2764	3		_	
56	42	53.8	2764	4	US-10-072-012-487		487, App
57	42	53.8	2764	5	US-10-631-467-1514		1514, Ap
58	42	53.8	2765	3	US-09-808-602-84		84, Appl
59	42	53.8	2765	3	US-09-800-198-72		72, Appl
60	42	53.8	2765	4	US-10-072-012-488		488, App
61	42	53.8	2765	5	US-10-453-372-116		116, App
62	42	53.8	2769	4	US-10-383-201-44	Sequence	44, Appl

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title: US-10-001-938-21

Perfect score: 78

1 DGQLKSVTINGVPDD 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06 NEW_PUB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

> 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:* 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

> /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	78	100.0	15	6	US-10-490-949-30	Sequence 30, Appl
2	38	48.7	230	6	US-10-953-349-6513	Sequence 6513, Ap
3	38	48.7	394	6	US-10-953-349-6512	Sequence 6512, Ap
4	37	47.4	216	6	US-10-953-349-5948	Sequence 5948, Ap
5	37	47.4	237	7	US-11-293-697-4647	Sequence 4647, Ap
6	37	47.4	239	6	US-10-953-349-5947	Sequence 5947, Ap
7	36	46.2	301	6	US-10-953-349-18989	Sequence 18989, A
8	36	46.2	351	7	US-11-293-697-2554	Sequence 2554, Ap
9	36	46.2	507	6	US-10-953-349-19123	Sequence 19123, A
10	36	46.2	593	6	US-10-953-349-19122	Sequence 19122, A
11	35.5	45.5	1270	6	US-10-532-050-1	Sequence 1, Appli
12	35	44.9	176	6	US-10-953-349-33303	Sequence 33303, A
13	35	44.9	262 347	6 6	US-10-953-349-11266 US-10-953-349-19220	Sequence 11266, A
14	35	44.9 44.9	347	6	US-10-953-349-11265	Sequence 19220, A Sequence 11265, A
15 16	35 35	44.9	336	6	US-10-953-349-11264	Sequence 11264, A
17	35	44.9	465	6	US-10-953-349-19219	Sequence 19219, A
18	35	44.9	483	6	US-10-953-349-11378	Sequence 11378, A
19	35	44.9	543	7	US-11-293-697-2444	Sequence 2444, Ap
20	34.5	44.2	630	7	US-11-293-697-2818	Sequence 2818, Ap
21	34	43.6	80	7	US-11-219-563-124	Sequence 124, App
22	34	43.6	167	6	US-10-953-349-23114	Sequence 23114, A
23	34	43.6	168	6	US-10-953-349-23113	Sequence 23113, A
24	34	43.6	192	6	US-10-953-349-25874	Sequence 25874, A
25	34	43.6	215	6	US-10-953-349-23112	Sequence 23112, A
26	34	43.6	217	6	US-10-953-349-21574	Sequence 21574, A
27	34	43.6	230	6	US-10-953-349-28783	Sequence 28783, A
28	34	43.6	235	6	US-10-953-349-13359	Sequence 13359, A
29	34	43.6		6	US-10-953-349-25873	Sequence 25873, A
30	34	43.6	242	6	US-10-953-349-25872	Sequence 25872, A
31	34	43.6	249	6	US-10-953-349-1158	Sequence 1158, Ap
32	34	43.6	249	6	US-10-953-349-33772	Sequence 33772, A
33	34	43.6	250	6	US-10-953-349-1157	Sequence 1157, Ap
34	34	43.6	255	6	US-10-953-349-19535	Sequence 19535, A
35	34	43.6		6	US-10-953-349-13358	Sequence 13358, A
36	34	43.6		6	US-10-953-349-13357	Sequence 13357, A
37	34	43.6		6 6	US-10-953-349-19534 US-10-953-349-19533	Sequence 19534, A Sequence 19533, A
38	34	43.6	306	_	US-10-953-349-21974	Sequence 21974, A
39 40	34 34	43.6 43.6		6 6	US-10-953-349-22074	Sequence 22074, A
41	34	43.6		6	US-10-953-349-21573	Sequence 21573, A
42	34	43.6		7	US-11-121-154-174	Sequence 174, App
43	34	43.6		6	US-10-953-349-21973	Sequence 21973, A
44	34	43.6		6	US-10-953-349-22073	Sequence 22073, A
45	34	43.6			US-10-953-349-21572	Sequence 21572, A
46	34	43.6			US-10-953-349-21972	Sequence 21972, A
47	34	43.6	392	6	US-10-953-349-22072	Sequence 22072, A
48	34	43.6	400	6	US-10-953-349-9203	Sequence 9203, Ap
49	34	43.6			US-10-953-349-9202	Sequence 9202, Ap
50	34	43.6	532	6	US-10-505-928-499	Sequence 499, App
51	33.5	42.9			US-11-313-356-3	Sequence 3, Appli
52	33	42.3			US-11-219-563-8	Sequence 8, Appli
53	33	42.3			US-11-219-121-16	Sequence 16, Appl
54	33	42.3			US-10-953-349-40090	Sequence 40090, A
55	33	42.3			US-10-953-349-34327	Sequence 34327, A
56 57	33	42.3			US-11-106-014-60	Sequence 60, Appl
57 50	33	42.3			US-10-511-937-2998	Sequence 2998, Ap Sequence 33145, A
58 50	33	42.3			US-10-953-349-33145	Sequence 33145, A Sequence 4567, Ap
59	33	42.3	335	6	US-10-953-349-4567	bequeite 4501, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-22.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 22.rai.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:37:25; Search time 14.6053 Seconds

(without alignments)

89.896 Million cell updates/sec

Title: US-10-001-938-22

Perfect score: 70

Sequence: 1 DLQLAMAYSLSEMEA 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1 2	. •	100.0	277 277		US-08-868-288A-7 US-09-235-373-7	Sequence 7, Appli Sequence 7, Appli

3	70	100.0	277	2	US-09-388-993-7	Sequence 7, Appli
4	70	100.0	277	2	US-09-501-714-7	Sequence 7, Appli
5	70	100.0	327	2	US-09-949-016-11262	Sequence 11262, A
6	70	100.0	351	1	US-08-868-288A-6	Sequence 6, Appli
7	70	100.0	351	2	US-09-235-373-6	Sequence 6, Appli
8	70	100.0	351	2	US-09-388-993-6	Sequence 6, Appli
9	70	100.0	351	2	US-09-501-714-6	Sequence 6, Appli
10	45	64.3	668	2	US-09-538-092-599	Sequence 599, App
11	40	57.1	698	2	US-09-710-279-2388	Sequence 2388, Ap
12	40	57.1	905	2	US-09-134-001C-3782	Sequence 3782, Ap
13	39	55.7	642	2	US-09-949-016-10283	Sequence 10283, A
14	39	55.7	690	2	US-08-971-089-6	Sequence 6, Appli
15	39	55.7	690	2	US-10-117-604A-6	Sequence 6, Appli
16	39	55.7	776	2	US-09-266-225D-10	Sequence 10, Appl
17	39	55.7	777	2	US-09-949-016-6540	Sequence 6540, Ap
18	38	54.3	472	2	US-08-976-255-17	Sequence 17, Appl
19	36	51.4	164	2	US-09-134-001C-5216	Sequence 5216, Ap
20	36	51.4	425	2	US-09-543-681A-7042	Sequence 7042, Ap
21	36	51.4	508	2	US-10-104-047-2186	Sequence 2186, Ap
22	36	51.4	813	2	US-09-964-899-25	Sequence 25, Appl
23	36	51.4	896	1	US-08-095-737-2	Sequence 2, Appli
24	36	51.4	896	1	US-08-480-145-2	Sequence 2, Appli
25	36	51.4	896	1	US-08-477-389-2	Sequence 2, Appli
26	36	51.4	896	2	US-09-538-092-1113	Sequence 1113, Ap
27	36	51.4	896	2	US-09-949-016-6155	Sequence 6155, Ap
28	36	51.4	897	1	US-08-095-737-4	Sequence 4, Appli
29	36	51.4	897	1	US-08-480-145-4	Sequence 4, Appli
30	36	51.4	897	ī	US-08-477-389-4	Sequence 4, Appli
31	36	51.4	926	2	US-09-949-016-10683	Sequence 10683, A
32	35	50.0	119	2	US-09-513-999C-5848	Sequence 5848, Ap
33	35	50.0	155	2	US-09-710-279-344	Sequence 344, App
34	35	50.0	225	2	US-09-543-681A-4987	Sequence 4987, Ap
35	35	50.0	436	2	US-09-902-540-16648	Sequence 16648, A
36	35	50.0	541	2	US-09-252-991A-21132	Sequence 21132, A
37	35	50.0	632	2	US-09-859-961-2	Sequence 2, Appli
38	35	50.0	832	2	US-10-464-939-2	Sequence 2, Appli
39	35	50.0	1058	2	US-10-464-939-4	Sequence 4, Appli
40	35	50.0	1121	2	US-09-949-016-11048	Sequence 11048, A
41	34.5	49.3	486	2	US-09-489-039A-8181	Sequence 8181, Ap
42	34.3	48.6	98	2	US-09-270-767-57849	Sequence 57849, A
43	34	48.6	131	2	US-09-270-767-31762	Sequence 31762, A
44	34	48.6	131	2	US-09-270-767-46979	Sequence 46979, A
45	34	48.6	218	2	US-09-543-681A-7325	Sequence 7325, Ap
46	34	48.6	288	2	US-09-134-000C-5520	Sequence 5520, Ap
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51	34	48.6	476	2	US-09-270-767-42546	Sequence 42546, A
52	34	48.6	478	2	US-09-716-964B-142	Sequence 142, App
53	34	48.6	557	2	US-09-248-796A-15455	Sequence 15455, A
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55	34	48.6	601	2	US-09-902-540-11118	Sequence 11118, A
56	34	48.6	601	2	US-09-902-540-15407	Sequence 15407, A
57	34	48.6	716	1	US-08-372-652-4	Sequence 4, Appli
58	34	48.6	716	5	PCT-US95-16311-4	Sequence 4, Appli
59	34	48.6	774	2	US-09-252-991A-29487	Sequence 29487, A
60	34	48.6	923	2	US-09-252-991A-27148	Sequence 27148, A
61	34	48.6	2172	1	US-08-611-107-31	Sequence 31, Appl
62	34	48.6	2257	1	US-08-611-107-10	Sequence 10, Appl
63	34	48.6	2257	1	US-08-422-560A-10	Sequence 10, Appl

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-22.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 938-22.rapbm.

<u>start</u>

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:58:51; Search time 63.3553 Seconds

(without alignments)

109.671 Million cell updates/sec

Title:

US-10-001-938-22

Perfect score: 70

Sequence: 1 DLQLAMAYSLSEMEA 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters:

2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA Main:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

용 Query

No. Score Match Length DB ID

Description

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3	41	58.6	18	4	US-10-193-452-86		86, Appl
4	41	58.6	64	3	US-09-864-761-33889	Sequence	33889, A
5	41	58.6	71	4	US-10-424-599-277428	Sequence	277428,
6	41	58.6	117	4	US-10-108-260A-2985	Sequence	2985, Ap
7	41	58.6	590	4	US-10-275-595A-33		33, Appl
8	40	57.1	232	4	US-10-311-035-1		1, Appli
9	40	57.1	443	5	US-10-450-763-58647		58647, A
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					• • • • • • • • • • • • • • • • • • • •	•	•
12	40	57.1	876	4	US-10-282-122A-70369	_	70369, A
13	40	57.1	876	4	US-10-282-122A-70998	-	70998, A
14	40	57.1	876	5	US-10-857-625-697	-	697, App
15	40	57.1	905	4	US-10-724-972A-6007	Sequence	6007, Ap
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17	40	57.1	980	4	US-10-399-645-6	Sequence	6, Appli
18	40	57.1	980	6	US-11-037-243-65		65, Appl
19	39	55.7	44	4	US-10-767-701-50107		50107, A
20	39	55.7	325	4	US-10-425-115-264787	Sequence	
21	39	55.7	461	4	US-10-425-115-264789	Sequence	
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22	39	55.7		4	US-10-425-114-55229	-	55229, A
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26	39	55.7	777	4	US-10-257-021-37	Sequence	37, Appl
27	38	54.3	875	4	US-10-282-122A-60678	Sequence	60678, A
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31	38	54.3	1431	5	US-10-840-512-218		218, App
32	38	54.3	1615	4	US-10-343-710-108		108, App
33	37	52.9	220	4	US-10-369-493-23007		23007, A
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35		52.9		_	US-10-282-122A-77695		77695, A
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37	37	52.9	813	6	US-11-097-143-40635	•	40635, A
38	36	51.4	164	4	US-10-724-972A-4287		4287, Ap
39	36	51.4	170	3	US-09-925-297-575		575, App
40	36	51.4	258	5	US-10-739-930-7937		7937, Ap
41	36	51.4	308	6	US-11-098-686-11286	Sequence	11286, A
42	36	51.4	321	6	US-11-156-084-168	Sequence	168, App
43	36	51.4	370	4	US-10-425-115-363269	Sequence	363269,
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50	36	51.4	813	3	US-09-964-899-25		25, Appl
51	36	51.4	813	5	US-10-975-523-25	-	25, Appl
52	36	51.4	824	6	US-11-097-143-10065		10065, A
53	36	51.4	824	6	US-11-097-143-10092		10092, A
54	36	51.4	952	4	US-10-369-493-5327	Sequence	5327, Ap
55	36	51.4	1101	6	US-11-097-143-9564	Sequence	9564, Ap
56	36	51.4	1369	4	US-10-437-963-184093	Sequence	184093,
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58	36	51.4	1809	5	US-10-745-237-54		54, Appl
59	36	51.4	1809	6	US-11-097-143-13683		13683, A
60	35	50.0	55	4	US-10-424-599-195544	Sequence	
61	35	50.0	57	4	US-10-425-115-308575	Sequence	
0 1	JJ	30.0	٥,	7	05 10 425 115-500575	bequeince	2000,0,

SCORE Search Results Details for Application 10 and Search Result us-10-001-938-22.rapl

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Go B

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OM protein - protein search, using sw model

June 2, 2006, 19:45:07; Search time 3.55263 Seconds

(without alignments)

48.831 Million cell updates/sec

Title: US-10-001-938-22

Perfect score: 70

Sequence: 1 DLQLAMAYSLSEMEA 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

58871 segs, 11565156 residues Searched:

58871 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1	70 41	100.0	15	6	US-10-490-949-31 US-11-293-697-2985	Sequence 31, Appl Sequence 2985, Ap

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3	38	54.3	1460	7	US-11-247-437-14		14, Appl
4	35	50.0	284	6	US-10-953-349-24383	•	24383, A
5	35	50.0	296	6	US-10-953-349-24382	Sequence	24382, A
6	35	50.0	318	6	US-10-953-349-24381	Sequence	24381, A
7	34	48.6	352	7	US-11-293-697-4023	Sequence	4023, Ap
8	34	48.6	468	6	US-10-953-349-3782		3782, Ap
9	34	48.6	499	6	US-10-953-349-3781		3781, Ap
10	34	48.6	552	6	US-10-953-349-3780		3780, Ap
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				-		_	9965, Ap
12	32	45.7	142	6	US-10-953-349-9964		9964, Ap
13	32	45.7	173	7	US-11-297-134-43	_	43, Appl
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15	32	45.7	230	6	US-10-953-349-999	Sequence	999, App
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17	32	45.7	340	6	US-10-953-349-2038	Sequence	2038, Ap
18	32	45.7	365	6	US-10-953-349-998	Sequence	998, App
19	32	45.7	369	6	US-10-953-349-997		997, App
20	32	45.7	414	6	US-10-953-349-4342		4342, Ap
21	32	45.7	465	6	US-10-953-349-4341		4341, Ap
22	32	45.7	466	6	US-10-953-349-4340		4340, Ap
23	32	45.7	468	6	US-10-953-349-23758		23758, A
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	32		2177	6	US-10-713-648A-64		64, Appl
25	31	44.3	213	6	US-10-953-349-8603	-	8603, Ap
26	31	44.3	232	6	US-10-953-349-20350	-	20350, A
27	31	44.3	260	6	US-10-953-349-20349	-	20349, A
28	31	44.3	317	6	US-10-953-349-21703	Sequence	21703, A
29	31	44.3	328	6	US-10-953-349-21702	Sequence	21702, A
30	31	44.3	345	6	US-10-953-349-21701	Sequence	21701, A
31	31	44.3	348	6	US-10-953-349-34772	Sequence	34772, A
32	31	44.3	350	6	US-10-953-349-34771	-	34771, A
33	31	44.3	352	6	US-10-953-349-34770	_	34770, A
34	31	44.3	779	6	US-10-531-965-2	-	2, Appli
35	30.5	43.6	1073	6	US-10-713-648A-54		54, Appl
36	30	42.9	241	6	US-10-953-349-1750		1750, Ap
37	30	42.9	253	6	US-10-953-349-39827		39827, A
38	30	42.9	258	6	US-10-953-349-18067		18067, A
39	30	42.9	262	6	US-10-953-349-26345		26345, A
40	30	42.9	316	6	US-10-953-349-26344		26344, A
41	30	42.9	316	6	US-10-953-349-39826		39826, A
42	30	42.9	323	6	US-10-953-349-39825		39825, A
43	30	42.9	333	6	US-10-953-349-23660		23660, A
44	30	42.9	356	6	US-10-953-349-23659	Sequence	23659, A
45	30	42.9	444	6	US-10-953-349-21229	Sequence	21229, A
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47	30	42.9	487	6	US-10-953-349-21227	Sequence	21227, A
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57	29	41.4	139	6	US-10-953-349-38612		38612, A
58	29	41.4	154	6	US-10-953-349-20540	_	20540, A
59	29	41.4	181	6	US-10-953-349-8622		8622, Ap
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61	29	41.4	183	6	US-10-953-349-27141	Sequence	27141, A
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63	29	41.4	193	6	US-10-953-349-1101	Sequence	1101, Ap
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SCORE Search Results Details for Application 10 and Search Result us-10-001-938-23.rai.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:12:07; Search time 12.7 Seconds

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-23

Perfect score: 76

Sequence: 1 EDLFMCMDIQLVEAL 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
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4	76	100 0	207	^	*** 00 010 030 170	Common 170 Pro-
4	76	100.0	397	2	US-09-919-039-178	Sequence 178, App
5	76	100.0	397	2	US-09-538-092-1052	Sequence 1052, Ap
6	76	100.0	397	2	US-09-501-714-5	Sequence 5, Appli
7	41	53.9	397	3	US-10-429-223-2	Sequence 2, Appli
8	41	53.9	397	3	US-10-429-223-4	Sequence 4, Appli
9	40	52.6	239	2	US-10-104-047-2162	Sequence 2162, Ap
10	40	52.6	963	1	US-08-537-002A-3	Sequence 3, Appli
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13	39	51.3	405	2	US-09-608-285A-25	
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14	39	51.3	405	2	US-09-370-265-25	Sequence 25, Appl
15	39	51.3	405	2	US-09-557-800C-25	Sequence 25, Appl
16	39	51.3	405	2	US-09-370-625A-25	Sequence 25, Appl
17	39	51.3	428	2	US-09-608-285A-3	Sequence 3, Appli
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19	39	51.3	428	2	US-09-608-285A-7	Sequence 7, Appli
20	39	51.3	428	2	US-09-240-639-6	Sequence 6, Appli
21	39	51.3	428	2	US-09-240-639-9	Sequence 9, Appli
22	39	51.3	428	2	US-09-350-836B-3	Sequence 3, Appli
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27	39	51.3	428	2	US-09-370-265-7	Sequence 7, Appli
28	39	51.3	428	2	US-09-557-800C-3	Sequence 3, Appli
29	39	51.3	428	2	US-09-557-800C-5	Sequence 5, Appli
30	39	51.3	428	2	US-09-557-800C-7	Sequence 7, Appli
31	39	51.3	428	2	US-09-370-625A-3	Sequence 3, Appli
32	39	51.3	428	2	US-09-370-625A-5	Sequence 5, Appli
33	39	51.3	428	2	US-09-370-625A-7	Sequence 7, Appli
34	39	51.3	428	2	US-09-908-510A-6	Sequence 6, Appli
35	39	51.3	428	2	US-09-908-510A-9	Sequence 9, Appli
36	39	51.3	428	2	US-09-905-744B-6	Sequence 6, Appli
37	39	51.3	428	2	US-09-905-744B-9	
38	39	51.3	428	2		Sequence 9, Appli
					US-10-107-660-6	Sequence 6, Appli
39	39	51.3	428	2	US-10-107-660-9	Sequence 9, Appli
40	39	51.3	428	2	US-10-107-576-6	Sequence 6, Appli
41	39	51.3	428	2	US-10-107-576-9	Sequence 9, Appli
42	39	51.3	428	2	US-09-905-732B-6	Sequence 6, Appli
43	39	51.3	428	2	US-09-905-732B-9	Sequence 9, Appli
44	39	51.3	428	2	US-09-949-016-6050	Sequence 6050, Ap
45	39	51.3	428	2	US-09-905-743B-6	Sequence 6, Appli
46	39	51.3	428	2	US-09-905-743B-9	Sequence 9, Appli
47	39	51.3	428	2	US-10-091-085-3	Sequence 3, Appli
48	39	51.3	428	2	US-10-091-085-5	Sequence 5, Appli
49	39	51.3	428	2	US-10-091-085-7	Sequence 7, Appli
50	39	51.3	428	2	US-09-905-589-6	Sequence 6, Appli
51	39	51.3	428	2		
					US-09-905-589-9	Sequence 9, Appli
52	39	51.3	428	2	US-10-108-171A-6	Sequence 6, Appli
53	39	51.3	428	2	US-10-108-171A-9	Sequence 9, Appli
54	39	51.3	470	2	US-09-949-016-11197	Sequence 11197, A
55	38	50.0	148	3	US-09-699-136B-2	Sequence 2, Appli
56	38	50.0	173	2	US-09-270-767-34380	Sequence 34380, A
57	38	50.0	173	2	US-09-270-767-49597	Sequence 49597, A
58	38	50.0	465	2	US-09-240-639-8	Sequence 8, Appli
59	38	50.0	465	2	US-09-557-800C-56	Sequence 56, Appl
60	38	50.0	465	2	US-09-370-625A-39	Sequence 39, Appl
61	38	50.0	465	2	US-09-908-510A-8	Sequence 8, Appli
62	38	50.0	465	2	US-09-905-744B-8	Sequence 8, Appli
63	38	50.0	465	2	US-10-107-660-8	Sequence 8, Appli
64	38	50.0	465	2	US-10-107-576-8	Sequence 8, Appli
٠.	30	55.0	400	-	35 10 107 570 0	pedactice of white

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 23.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 23.rapbm.

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OM protein - protein search, using sw model

June 2, 2006, 19:45:16; Search time 63.4 Seconds Run on:

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-23

Perfect score: 76

Sequence: 1 EDLFMCMDIQLVEAL 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published_Applications_AA_Main:* Database :

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용 Result Query Description No. Score Match Length DB ID _____ 76 100.0 15 4 US-10-001-938-23 Sequence 23, Appl

2	76	100.0	258	5	US-10-473-127-1141	Sequence 1141, A	lp
3	76	100.0	258	5	US-10-473-127-1146	Sequence 1146, F	ď
4	76	100.0	397	3	US-09-919-039-178	Sequence 178, Ap	
5	76	100.0	397	5	US-10-473-127-1138		
						Sequence 1138, A	
6	76	100.0	397	5	US-10-473-127-1139	Sequence 1139, F	
7	76	100.0	397	5	US-10-473-127-1140	Sequence 1140, F	۱p
8	76	100.0	397	5	US-10-473-127-1143	Sequence 1143, F	lp
9	76	100.0	397	5	US-10-473-127-1144	Sequence 1144, A	
10	76	100.0	397	5	US-10-473-127-1145	Sequence 1145, F	-
	76						
11		100.0	397	5	US-10-756-149-4727	Sequence 4727, F	-
12	76	100.0	397	5	US-10-631-467-559	Sequence 559, Ap	
13	76	100.0	397	5	US-10-631-467-1386	Sequence 1386, F	٩
14	76	100.0	397	5	US-10-878-556A-155	Sequence 155, Ap	ac
15	76	100.0	408	5	US-10-450-763-40099	Sequence 40099,	_
16	46	60.5	403	6	US-11-097-143-24405	Sequence 24405,	
						-	
17	46	60.5	403	6	US-11-097-143-41904	Sequence 41904,	
18	42	55.3	538	4	US-10-424-599-218710	Sequence 218710,	
19	41	53.9	397	4	US-10-429-223-2	Sequence 2, Appl	.i
20	41	53.9	397	4	US-10-429-223-4	Sequence 4, Appl	
21	40	52.6	239	4	US-10-104-047-2162	Sequence 2162, F	
22	40	52.6	239			-	_
				6	US-11-072-512-2162	Sequence 2162, A	_
23	40	52.6	397	4	US-10-108-260A-3837	Sequence 3837, F	
24	40	52.6	426	4	US-10-108-260A-4751	Sequence 4751, A	γp
25	40	52.6	487	4	US-10-425-115-348539	Sequence 348539,	
26	40	52.6	524	4	US-10-369-493-6490	Sequence 6490, F	αA
27	40	52.6	542	4	US-10-437-963-123435	Sequence 123435,	_
28	39	51.3	194	4	US-10-369-493-17440	Sequence 17440,	
				_			
29	39	51.3	330	3	US-09-925-299-876	Sequence 876, Ap	
30	39	51.3	330	3	US-09-925-299-876	Sequence 876, Ap	
31	39	51.3	405	4	US-10-092-063-25	Sequence 25, App	1
32	39	51.3	405	4	US-10-286-926-25	Sequence 25, App	1
33	39	51.3	410	6	US-11-069-543-142	Sequence 142, Ar	
34	39	51.3	428	4	US-10-091-085-3	Sequence 3, Appl	-
35	39	51.3	428	4	US-10-091-085-5	Sequence 5, Appl	
36	39			4			
		51.3	428	-	US-10-091-085-7	Sequence 7, Appl	
37	39	51.3	428	4	US-10-092-063-3	Sequence 3, Appl	
38	39	51.3	428	4	US-10-092-063-5	Sequence 5, Appl	.i
39	39	51.3	428	4	US-10-092-063-7	Sequence 7, Appl	.i
40	39	51.3	428	4	US-10-286-926-3	Sequence 3, Appl	i
41	39	51.3	428	4	US-10-286-926-5	Sequence 5, Appl	
42	39	51.3	428	4	US-10-286-926-7	Sequence 7, Appl	
43	39			_			
		51.3	428	4	US-10-231-913-127	Sequence 127, Ap	
44	39	51.3	428	4	US-10-408-765A-2296	Sequence 2296, F	
45	39	51.3	428	6	US-11-069-543-175	Sequence 175, Ap	p
46	39	51.3	519	4	US-10-408-765A-410	Sequence 410, Ap	p
47	38	50.0	39	6	US-11-004-399-286	Sequence 286, Ap	q
48	38	50.0	39	6	US-11-004-399-617	Sequence 617, Ap	
49	38	50.0	39	6	US-11-004-399-3928	Sequence 3928, A	
50	38		76	4	US-10-425-115-213449	Sequence 213449,	
		50.0				-	
51	38	50.0	119	4	US-10-437-963-163481	Sequence 163481,	
52	38	50.0	148	3	US-09-942-407-2	Sequence 2, Appl	.i
53	38	50.0	148	4	US-10-371-475-2	Sequence 2, Appl	.i
54	38	50.0	148	4	US-10-829-897-2	Sequence 2, Appl	.i
55	38	50.0	186	6	US-11-097-143-33963	Sequence 33963,	
56	38	50.0	233	4	US-10-437-963-150553	Sequence 150553,	
57			407	-	US-10-437-963-150403	_	
	38	50.0		4		Sequence 150403,	
58	38	50.0	427	4	US-10-231-913-126	Sequence 126, Ar	
59	38	50.0	465	4	US-10-092-063-39	Sequence 39, App	
60	38	50.0	537	4	US-10-369-493-8024	Sequence 8024, A	۱p
61	38	50.0	560	6	US-11-097-143-39837	Sequence 39837,	Α
62	38	50.0	1080	4	US-10-322-281-626	Sequence 626, Ar	
_		-		-	· 	1	•

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-23.rapbn.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title: US-10-001-938-23

Perfect score: 76

Sequence: 1 EDLFMCMDIQLVEAL 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description	on
1	76	100.0	15	6	US-10-490-949-32	Sequence	32, Appl
2	40	52.6	397	7	US-11-293-697-3837		3837, Ap
3	40	52.6	426	7	US-11-293-697-4751		4751, Ap
4	36	47.4	257	6	US-10-953-349-1056	-	1056, Ap
5	36	47.4	278	6	US-10-953-349-33998		33998, A
6	36	47.4	288	6	US-10-953-349-33997		33997, A
7	36	47.4	313	6	US-10-953-349-33996		33996, A
8	36	47.4	337	6	US-10-953-349-1055		1055, Ap
9	36	47.4	338	6	US-10-953-349-13711	_	13711, A
10	36	47.4	375	6	US-10-953-349-6679		6679, Ap
11	36	47.4	382	6	US-10-953-349-13710		13710, A
12	36	47.4	419	6	US-10-953-349-1054	_	1054, Ap
13	36	47.4	420	6	US-10-953-349-13709		13709, A
14	36	47.4	431	6	US-10-953-349-6678	_	6678, Ap
15	36	47.4	442	6	US-10-953-349-6677		6677, Ap
16	35	46.1	842	7	US-11-266-446-68		68, Appl
17	34	44.7	191	6	US-10-953-349-12085		12085, A
18	34	44.7	358	7	US-11-293-697-2674		2674, Ap
19	34	44.7	364	6	US-10-196-749-572		572, App
20	34	44.7	621	7	US-11-293-697-4148		4148, Ap
21	33.5	44.1	240	6	US-10-953-349-24825		24825, A
22	33	43.4	117	6	US-10-953-349-29788	Sequence	29788, A
23	33	43.4	151	6	US-10-953-349-29786		29786, A
24	33	43.4	326	7	US-11-140-450-44		44, Appl
25	33	43.4	366	7	US-11-255-699-2	_	2, Appli
26	33	43.4	2871	6	US-10-505-928-100	_	100, App
27	32.5	42.8	175	6	US-10-953-349-14897		14897, A
28	32.5	42.8	253	6	US-10-953-349-14896		14896, A
29	32.5	42.8	296	6	US-10-953-349-14895		14895, A
30	32	42.1	147	7	US-11-293-697-2658	Sequence	2658, Ap
31	32	42.1	156	7	US-11-293-697-3460	Sequence	3460, Ap
32	32	42.1	175	7	US-11-075-398-2	Sequence	2, Appli
33	32	42.1	188	6	US-10-953-349-16220	Sequence	16220, A
34	32	42.1	234	6	US-10-953-349-16219	Sequence	16219, A
35	32	42.1	240	6	US-10-953-349-16218	Sequence	16218, A
36	32	42.1	286	6	US-10-953-349-30735	Sequence	30735, A
37	32	42.1	304	6	US-10-953-349-30734	Sequence	30734, A
38	32	42.1	311	6	US-10-953-349-16431		16431, A
39	32	42.1	326	6	US-10-953-349-9889	Sequence	9889, Ap
40	32	42.1	331	6	US-10-953-349-30733	-	30733, A
41	32	42.1	370	6	US-10-953-349-9888		9888, Ap
42	32	42.1	380	6	US-10-953-349-20050	Sequence	20050, A
43	32	42.1	391	6	US-10-953-349-20049		20049, A
44	32	42.1	406	6	US-10-953-349-9887		9887, Ap
45	32	42.1	434	6	US-10-953-349-19834	-	19834, A
46	32	42.1	443	6	US-10-953-349-19833		19833, A
47	32	42.1	475	6	US-10-953-349-19832	-	19832, A
48	32	42.1	529	6	US-10-953-349-16430	•	16430, A
49	32	42.1	536	6	US-10-953-349-16429		16429, A
50	32	42.1	821	6	US-10-505-928-316		316, App
51	32	42.1	847	6	US-10-505-928-495		495, App
52	31	40.8	226	6	US-10-953-349-35189		35189, A
53	31	40.8	244	6	US-10-953-349-26029	=	26029, A
54	31	40.8	254	7	US-11-266-747-1284	-	1284, Ap
55	31	40.8	254	7	US-11-266-747-1710		1710, Ap
56	31	40.8	256	6	US-10-953-349-16379		16379, A
57 50	31	40.8	259	6	US-10-953-349-35188		35188, A
58 50	31	40.8	267	6	US-10-953-349-35187		35187, A
59	31	40.8	291	6	US-10-953-349-3229	sequence	3229, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-24.rai.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:12:07; Search time 12.7 Seconds

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-24

Perfect score: 81

Sequence: 1 LCGFQKPISTLDNRT 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database: Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No. Score Match Length DB ID

Description

1	81	100.0	397	1	US-08-868-288A-5	Sequence 5, Appli
2	81	100.0	397	2	US-09-235-373-5	Sequence 5, Appli
3	81	100.0	397	2	US-09-388-993-5	Sequence 5, Appli
4	81	100.0	397	2	US-09-919-039-178	Sequence 178, App
5	81	100.0	397	2	US-09-538-092-1052	Sequence 1052, Ap
6	81	100.0	397	2	US-09-501-714-5	Sequence 5, Appli
7	60	74.1	239	2	US-10-104-047-2162	Sequence 2162, Ap
8	55	67.9	397	3	US-10-429-223-2	Sequence 2, Appli
9	55	67.9	397	3	US-10-429-223-4	Sequence 4, Appli
10	53	65.4	347	2	US-09-248-796A-19195	Sequence 19195, A
11	47	58.0	419	1	US-08-686-417-3	Sequence 3, Appli
12	43	53.1	76	2	US-09-252-991A-21761	Sequence 21761, A
13	42	51.9	186	2	US-09-780-016-14	Sequence 14, Appl
14	42	51.9	186	2	US-10-214-811-14	Sequence 14, Appl
15	42	51.9	186	2	US-10-766-074-14	Sequence 14, Appl
16	42	51.9	211	2	US-09-780-016-10	Sequence 10, Appl
17	42	51.9	211	2	US-10-214-811-10	Sequence 10, Appl
18	42	51.9	211	2	US-10-766-074-10	Sequence 10, Appl
19	42	51.9	242	2	US-09-780-016-16	Sequence 16, Appl
20	42	51.9	242	2	US-10-214-811-16	Sequence 16, Appl
21	42	51.9	242	2	US-10-766-074-16	Sequence 16, Appl
22	42	51.9	265	2	US-09-780-016-8	Sequence 8, Appli
23	42	51.9	265	2	US-10-214-811-8	Sequence 8, Appli
24	42	51.9	265	2	US-10-766-074-8	Sequence 8, Appli
25	42	51.9	267	2	US-09-780-016-12	Sequence 12, Appl
26	42	51.9	267	2	US-10-214-811-12	Sequence 12, Appl
27	42	51.9	267	2	US-10-766-074-12	Sequence 12, Appl
28	42	51.9	290	2	US-09-780-016-6	Sequence 6, Appli
29	42	51.9	290	2	US-10-214-811-6	Sequence 6, Appli
30	42	51.9	290	2	US-10-766-074-6	Sequence 6, Appli
31	42	51.9	428	2	US-09-780-016-22	Sequence 22, Appl
32	42	51.9	428	2	US-10-214-811-22	Sequence 22, Appl
33	42	51.9	428	2	US-10-766-074-22	Sequence 22, Appl
34	42	51.9	453	2	US-09-780-016-18	Sequence 18, Appl
35	42	51.9	453	2	US-10-214-811-18	Sequence 18, Appl
36	42	51.9	453	2	US-10-766-074-18	Sequence 18, Appl
37	42	51.9	484	2	US-09-780-016-26	Sequence 26, Appl
38	42	51.9	484	2	US-10-214-811-26	Sequence 26, Appl
39	42	51.9	484	2	US-10-766-074-26	Sequence 26, Appl
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41	42	51.9	507	2	US-10-214-811-2	Sequence 2, Appli
42	42	51.9	507	2	US-10-766-074-2	Sequence 2, Appli
43	42	51.9	509	2	US-09-780-016-24	Sequence 24, Appl
44	42	51.9	509	2	US-10-214-811-24	Sequence 24, Appl
45	42	51.9	509	2	US-10-766-074-24	Sequence 24, Appl
46	42	51.9	532	2	US-09-780-016-20	Sequence 20, Appl
47	42	51.9	532	2	US-10-214-811-20	Sequence 20, Appl
48	42	51.9	532	2	US-10-766-074-20	Sequence 20, Appl
49	41	50.6	150	2	US-09-270-767-44364	Sequence 44364, A
50	41	50.6	728	2	US-09-270-767-44662	Sequence 44662, A
51	40	49.4	96	2	US-09-513-999C-6655	Sequence 6655, Ap
52	39.5	48.8	1019	2	US-09-434-066-23	Sequence 23, Appl
53	39	48.1	320	2	US-09-489-039A-10349	Sequence 10349, A
54	39	48.1	340	1	US-08-974-546-5	Sequence 5, Appli
55	39	48.1	340	2	US-09-949-016-6691	Sequence 6691, Ap
56	39	48.1	343	2	US-09-328-352-6577	Sequence 6577, Ap
57	39	48.1	363	2	US-09-949-016-8899	Sequence 8899, Ap
58	38	46.9	100	2	US-08-311-731A-235	Sequence 235, App
59 60	38	46.9	328	2	US-09-328-352-4546	Sequence 4546, Ap
60	38	46.9	336	2	US-09-270-767-33924	Sequence 33924, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 24.rapbm.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 24.rapbm.

start

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-24

Perfect score: 81

Sequence: 1 LCGFQKPISTLDNRT 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용 Result Query No. Score Match Length DB ID Description ------81 100.0 15 4 US-10-001-938-24 Sequence 24, Appl

2	81	100.0	258	5	US-10-473-127-1141	Sequence	1141, Ap
3	81	100.0	258	5	US-10-473-127-1146	Sequence	1146, Ap
4	81	100.0	397	3	US-09-919-039-178	Sequence	
5	81	100.0	397	5	US-10-473-127-1138	Sequence	
6	81	100.0	397	5	US-10-473-127-1140	Sequence	
7	81	100.0	397	5	US-10-473-127-1144	Sequence	
8	81	100.0	397	5	US-10-473-127-1145	Sequence	1145, Ap
9	81	100.0	397	5	US-10-756-149-4727	Sequence	4727, Ap
10	81	100.0	397	5	US-10-631-467-559	Sequence	_
11	81	100.0	397	5	US-10-631-467-1386	Sequence	
12				5			
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13	81	100.0	408	5	US-10-450-763-40099		40099, A
14	76	93.8	397	5	US-10-473-127-1139	Sequence	1139, Ap
15	76	93.8	397	5	US-10-473-127-1143	Sequence	1143, Ap
16	60	74.1	239	4	US-10-104-047-2162	Sequence	2162, Ap
17	60	74.1	239	6	US-11-072-512-2162	Sequence	_
18	60	74.1	397	4	US-10-108-260A-3837	Sequence	-
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19	60	74.1	426	4	US-10-108-260A-4751	Sequence	
20	55	67.9	397	4	US-10-429-223-2	Sequence	
21	55	67.9	397	4	US-10-429-223-4	Sequence	4, Appli
22	53	65.4	403	6	US-11-097-143-24405	Sequence	24405, A
23	53	65.4	403	6	US-11-097-143-41904	Sequence	41904, A
24	48	59.3	418	4	US-10-425-115-307678	Sequence	
25	48	59.3	418	4	US-10-425-115-307679	Sequence	
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26	48	59.3	433	4	US-10-425-114-60908	_	60908, A
27	47	58.0	193	4	US-10-425-115-303421	Sequence	303421,
28	47	58.0	235	6	US-11-096-568A-16063	Sequence	16063, A
29	47	58.0	266	4	US-10-425-115-307674	Sequence	307674,
30	47	58.0	330	6	US-11-096-568A-16062	_	16062, A
31	47	58.0	336	6	US-11-096-568A-16061		16061, A
32	47	58.0	338	6	US-11-096-568A-21865		21865, A
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33	47	58.0	342	4	US-10-425-114-68558	_	68558, A
34	47	58.0	370	4	US-10-259-194A-44	Sequence	
35	47	58.0	417	4	US-10-437-963-194306	Sequence	194306,
36	47	58.0	417	4	US-10-425-115-307680	Sequence	307680,
37	47	58.0	419	4	US-10-437-963-194308	Sequence	194308,
38	47	58.0	419	4	US-10-767-701-47403		47403, A
39	47	58.0	419	4	US-10-425-115-266771	Sequence	
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	47	58.0	419	-	US-10-425-115-266773	-	•
41	47	58.0	419	4	US-10-425-115-266781	Sequence	
42	47	58.0	419	4	US-10-425-115-305086	Sequence	305086,
43	47	58.0	419	6	US-11-096-568A-21864	Sequence	21864, A
44	47	58.0	420	4	US-10-425-115-266776	Sequence	266776,
45	47	58.0	421	4	US-10-425-114-63525	_	63525, A
46	47	58.0	449	4	US-10-425-114-62758	_	62758, A
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47	47	58.0	449	4	US-10-425-114-63503		63503, A
48	47	58.0	449	4	US-10-425-114-65975		65975, A
49	47	58.0	449	4	US-10-425-114-73027	Sequence	73027, A
50	47	58.0	450	4	US-10-425-114-46482	Sequence	46482, A
51	47	58.0	450	4	US-10-425-114-51073	Sequence	51073, A
52	47	58.0	450	4	US-10-425-114-66222	_	66222, A
53	47	58.0	450	4	US-10-425-114-67773	_	67773, A
54	47	58.0	455	4	US-10-425-114-53631		53631, A
55	47	58.0	463	4	US-10-425-114-46997	_	46997, A
56	47	58.0	465	4	US-10-425-114-59416	-	59416, A
57	47	58.0	465	4	US-10-425-114-60884	Sequence	60884, A
58	47	58.0	465	4	US-10-425-114-63473	•	63473, A
59	47	58.0	468	4	US-10-425-114-66072		66072, A
60	47	58.0	469	4	US-10-425-114-62592		62592, A
							65844, A
61	47	58.0	469	4	US-10-425-114-65844		
62	47	58.0	471	4	US-10-425-114-69286	sequence	69286, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-24.rapbn.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-24.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-24

Perfect score: 81

Sequence:

1 LCGFQKPISTLDNRT 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters:

58871

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:* 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Descriptio	n
1	81	100.0	15	 6	US-10-490-949-33	Sequence	33. Appl
2	60	74.1	397	7	US-11-293-697-3837	Sequence	
3	60	74.1	426	7	US-11-293-697-4751	Sequence	
4	43.5	53.7	792	6	US-10-953-349-38485		38485, A
5	43.5	53.7	805	6	US-10-953-349-38484	Sequence	38484, A
6	43.5	53.7	857	6	US-10-953-349-38483	Sequence	38483, A
7	42	51.9	256	6	US-10-953-349-16379	Sequence	16379, A
8	42	51.9	336	6	US-10-953-349-16378	Sequence	16378, A
9	42	51.9	338	6	US-10-953-349-13711	Sequence	13711, A
10	42	51.9	382	6	US-10-953-349-13710	Sequence	13710, A
11	42	51.9	417	6	US-10-953-349-16377	Sequence	
12	42	51.9	420	6	US-10-953-349-13709	Sequence	
13	41	50.6	257	6	US-10-953-349-1056	Sequence	-
14	41	50.6	337	6	US-10-953-349-1055	Sequence	_
15	41	50.6	419	6	US-10-953-349-1054	Sequence	
16	41	50.6	487	6	US-10-953-349-953	Sequence	
17	41	50.6	546	6	US-10-953-349-952	Sequence	
18	39	48.1	189	6	US-10-953-349-29757	Sequence	
19	39	48.1	210	6	US-10-953-349-29756	Sequence	
20 21	39	48.1 46.9	241	6	US-10-953-349-29755	Sequence	
22	38 38	46.9	307 335	6 6	US-10-953-349-2183 US-10-953-349-2182	Sequence	
23	36 38	46.9	343	6	US-10-953-349-2182 US-10-953-349-2181	Sequence Sequence	-
24	35	43.2	109	6	US-10-953-349-2161 US-10-953-349-13281		•
25	35	43.2	121	6	US-10-953-349-13280	Sequence	13281, A
26	35	43.2	131	6	US-10-953-349-13279	Sequence	
27	35	43.2	139	6	US-10-953-349-12099	Sequence	
28	35	43.2	153	7	US-11-293-697-3623	Sequence	
29	35	43.2	155	6	US-10-953-349-12098	_	12098, A
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31	35	43.2	357	6	US-10-953-349-19869	Sequence	
32	35	43.2	380	6	US-10-953-349-19868	Sequence	
33	35	43.2	388	6	US-10-953-349-19867	Sequence	
34	35	43.2	786	7	US-11-177-635-8	Sequence	
35	34	42.0	168	6	US-10-953-349-18747	Sequence	
36	34	42.0	171	6	US-10-953-349-18746	Sequence	18746, A
37	34	42.0	211	6	US-10-953-349-18745	Sequence	18745, A
38	34	42.0	336	6	US-10-953-349-5628	Sequence	
39		42.0	383	6		•	18444, A
40	34	42.0	400	6	US-10-953-349-18443		18443, A
41	34	42.0	483	6	US-10-953-349-11378		11378, A
42	34	42.0	512	7	US-11-293-697-4080	Sequence	-
43	34	42.0	523	6	US-10-953-349-20058	Sequence	
44	34	42.0	545	6	US-10-953-349-20057	Sequence	
45	34	42.0	557	6	US-10-953-349-20056	-	20056, A
46	33.5	41.4	211	6	US-10-953-349-12022	Sequence	
47	33.5	41.4	377	6	US-10-953-349-12021	Sequence	
48	33	40.7	126	6	US-10-953-349-15907		15907, A
49	33	40.7	158	6	US-10-953-349-9661	Sequence	
50 51	33	40.7	160	6	US-10-953-349-28747	_	28747, A
51 52	33 33	40.7 40.7	162 168	6	US-10-953-349-15906 US-10-953-349-9660		15906, A 9660, Ap
52 53	33	40.7	170	6 6	US-10-953-349-9660 US-10-953-349-15905	_	-
53 54	33	40.7	184	6	US-10-953-349-15905 US-10-953-349-28745	Sequence Sequence	15905, A
55	33	40.7	221	6	US-10-953-349-28745 US-10-953-349-11731		28745, A 11731, A
56	33	40.7	222	6	US-10-953-349-11731 US-10-953-349-11730		11731, A 11730, A
57	33	40.7	226		US-10-505-928-193		193, App
58	33	40.7	308	6	US-10-953-349-33811		33811, A
59	33	40.7	317	6	US-10-953-349-11729	-	11729, A
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SCORE Search Results Details for Application 100 and Search Result us-10-001-938-25.rai.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 25.rai.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:37:25; Search time 14.6053 Seconds

(without alignments)

89.896 Million cell updates/sec

Title: US-10-001-938-25

Perfect score: 78

Sequence: 1 RTIVITSHPGQIVKH 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1 2	78 78	100.0	397 397		US-08-868-288A-5 US-09-235-373-5	Sequence 5, Appli Sequence 5, Appli

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3	78	100.0	397	2	US-09-388-993-5	Sequence	5, Appli
4	78	100.0	397	2	US-09-919-039-178	Sequence	178, App
5	78	100.0	397	2	US-09-538-092-1052	Sequence	1052, Ap
6	78	100.0	397	2	US-09-501-714-5	_	5, Appli
7	49	62.8	397	3	US-10-429-223-2		2, Appli
8	49	62.8	397	3	US-10-429-223-4	-	
							4, Appli
9	48	61.5	239	2	US-10-104-047-2162		2162, Ap
10	44	56.4	26	2	US-10-057-789-126		126, App
11	44	56.4	27	2	US-10-057-789-128	Sequence	128, App
12	43	55.1	198	2	US-09-270-767-41637	Sequence	41637, A
13	42	53.8	155	2	US-09-087-134-12		12, Appl
14	42	53.8	228	2	US-09-949-002-409	-	409, App
15	42	53.8	267	2	US-09-328-352-6820		6820, Ap
16	42	53.8	518	2	US-09-113-309-19	_	19, Appl
17	42	53.8	518	2	US-09-521-109-19	_	19, Appl
18	42	53.8	518	2	US-09-562-332-19	Sequence	19, Appl
19	42	53.8	534	2	US-09-087-134-11	Sequence	11, Appl
20	42	53.8	824	2	US-09-949-002-312	Sequence	312, App
21	41	52.6	43	2	US-09-270-767-61905		61905, A
22	41	52.6	326	2	US-09-270-767-46335		46335, A
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23	41	52.6	522	2	US-09-489-039A-10041	-	10041, A
24	40	51.3	266	2	US-09-949-016-8843	_	8843, Ap
25	40	51.3	266	2	US-09-949-016-8844	Sequence	8844, Ap
26	40	51.3	397	1	US-08-371-377-19	Sequence	19, Appl
27	40	51.3	397	2	US-08-875-553D-25	Sequence	25, Appl
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29	40	51.3	398	2	US-08-875-553D-23	_	23, Appl
30	40	51.3	419	1	US-08-686-417-3	_	
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31	40	51.3	462	1	US-08-299-351-1	_	1, Appli
32	40	51.3	462	1	US-08-371-377-18	Sequence	18, Appl
33	40	51.3	462	2	US-09-309-572-10	Sequence	10, Appl
34	40	51.3	462	2	US-09-718-096-10	Sequence	10, Appl
35	40	51.3	462	2	US-08-875-553D-24		24, Appl
36	40	51.3	462	2	US-09-949-016-6075	_	6075, Ap
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41	40	51.3	478	2	US-09-949-016-7819	Sequence	7819, Ap
42	40	51.3	510	2	US-09-252-991A-33009	Sequence	33009, A
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45	39	50.0	460	2	US-09-248-796A-19819		19819, A
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48	39	50.0	1159	2	US-09-351-215-13		13, Appl
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50	39	50.0	1159	2	US-09-226-012-4	Sequence	4, Appli
51	39	50.0	1159	2	US-09-358-383C-10	Sequence	10, Appl
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53	38.5	49.4	576	2	US-09-328-352-7413	_	7413, Ap
54	38	48.7	70	2	US-09-107-433-4651		4651, Ap
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55	38	48.7	151	2	US-09-583-110-3331		3331, Ap
56	38	48.7	326	2	US-09-134-000C-5365		5365, Ap
57	38	48.7	420	2	US-09-213-053-4	-	4, Appli
58	38	48.7	426	2	US-09-248-796A-15263	Sequence	15263, A
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62	38	48.7	1060	2	US-09-248-796A-18062		18062, A
63	38	48.7	1394	2	US-09-213-053-2	sequence	2, Appli

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 25.rapbm.

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OM protein - protein search, using sw model

June 2, 2006, 19:58:51; Search time 63.3553 Seconds Run on:

(without alignments)

109.671 Million cell updates/sec

Title: US-10-001-938-25

Perfect score: 78

Sequence: 1 RTIVITSHPGQIVKH 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published_Applications_AA_Main:* Database :

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SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-25.rapbn.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:45:07; Search time 3.55263 Seconds

(without alignments)

48.831 Million cell updates/sec

Title:

US-10-001-938-25

Perfect score: 78

Sequence:

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Gapop 10.0, Gapext 0.5

Searched:

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Total number of hits satisfying chosen parameters:

58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

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SUMMARIES

Result

Query

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53 34 43.6 163 7 US-11-249-111-107 Sequence 107, App 54 34 43.6 194 6 US-10-510-162-4 Sequence 4, Appli 55 34 43.6 195 6 US-10-953-349-2234 Sequence 2234, Ap 56 34 43.6 195 6 US-10-953-349-37209 Sequence 37209, A 57 34 43.6 198 6 US-10-953-349-2233 Sequence 2233, Ap 58 34 43.6 198 6 US-10-953-349-37208 Sequence 37208, A							
54 34 43.6 194 6 US-10-510-162-4 Sequence 4, Appli 55 34 43.6 195 6 US-10-953-349-2234 Sequence 2234, Ap 56 34 43.6 195 6 US-10-953-349-37209 Sequence 37209, A 57 34 43.6 198 6 US-10-953-349-2233 Sequence 2233, Ap 58 34 43.6 198 6 US-10-953-349-37208 Sequence 37208, A							
55 34 43.6 195 6 US-10-953-349-2234 Sequence 2234, Ap 56 34 43.6 195 6 US-10-953-349-37209 Sequence 37209, A 57 34 43.6 198 6 US-10-953-349-2233 Sequence 2233, Ap 58 34 43.6 198 6 US-10-953-349-37208 Sequence 37208, A					_		
56 34 43.6 195 6 US-10-953-349-37209 Sequence 37209, A 57 34 43.6 198 6 US-10-953-349-2233 Sequence 2233, Ap 58 34 43.6 198 6 US-10-953-349-37208 Sequence 37208, A		34	43.6	195	6	US-10-953-349-2234	
58 34 43.6 198 6 US-10-953-349-37208 Sequence 37208, A					6		Sequence 37209, A
59 34 43.6 214 6 US-10-953-349-37207 Sequence 37207, A							
	59	34	43.6	214	6	US-10-953-349-37207	Sequence 37207, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-26

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:08:52; Search time 11.4238 Seconds

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-26

Perfect score: 79

Sequence: 1 GRLIIEFKVNFPENG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1 2	79 79	100.0	397 397	1 2	US-08-868-288A-5 US-09-235-373-5	Sequence 5, Appli Sequence 5, Appli

3	79	100.0	397	2	US-09-388-993-5	Sequence	5, Appli
4	79	100.0	397	2	US-09-919-039-178	Sequence	178, App
5	79	100.0	397	2	US-09-538-092-1052		1052, Ap
6	79	100.0	397	2	US-09-501-714-5	-	5, Appli
7			397				
	52	65.8		2	US-09-248-796A-17628	_	17628, A
8	50	63.3	348	1	US-08-974-546-1	_	1, Appli
9	47	59.5	340	1	US-08-974-546-5	Sequence	5, Appli
10	47	59.5	340	2	US-09-949-016-6691	Sequence	6691, Ap
11	47	59.5	363	2	US-09-949-016-8899	•	8899, Ap
12	46	58.2	334	3	US-10-429-223-3	-	3, Appli
13	46	58.2	337	2	US-09-665-479A-8	-	8, Appli
14	45	57.0	77	2	US-09-270-767-57315		57315, A
15	45	57.0	128	2	US-09-270-767-42059	Sequence	42059, A
16	43	54.4	666	2	US-09-134-001C-5465	Sequence	5465, Ap
17	42	53.2	86	1	US-08-785-795-1	-	1, Appli
18	42	53.2	397	3	US-10-429-223-2	-	2, Appli
						-	
19	41	51.9	96	2	US-09-248-796A-21503	_	21503, A
20	41	51.9	662	2	US-09-583-110-4571	Sequence	4571, Ap
21	41	51.9	679	2	US-09-107-433-3402	Sequence	3402, Ap
22	40.5	51.3	74	2	US-09-270-767-57464	Sequence	57464, A
23	40.5	51.3	262	2	US-09-270-767-42193		42193, A
24	40	50.6	239	2	US-10-104-047-2162	_	2162, Ap
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25	40	50.6	358	1	US-08-868-288A-1		1, Appli
26	40	50.6	358	2	US-09-235-373-1		1, Appli
27	40	50.6	358	2	US-09-388-993-1	Sequence	1, Appli
28	40	50.6	358	2	US-09-991-181-148	Sequence	148, App
29	40	50.6	358	2	US-09-501-714-1	=	1, Appli
30	40	50.6	358	2	US-09-990-444-148		148, App
						_	
31	40	50.6	358	2	US-09-997-333-148	_	148, App
32	40	50.6	358	2	US-09-992-598-148	_	148, App
33	40	50.6	358	2	US-09-989-735-148	Sequence	148, App
34	40	50.6	358	3	US-09-989-726-148	Sequence	148, App
35	40	50.6	358	3	US-09-997-514-148	_	148, App
36	40	50.6	358	3	US-09-989-728-148		148, App
37	40	50.6	358	3	US-09-997-349-148		148, App
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38	40	50.6	358	3	US-09-997-653-148	_	148, App
39	40	50.6	358	3	US-09-989-293A-148		148, App
40	40	50.6	419	1	US-08-686-417-3	Sequence	3, Appli
41	40	50.6	428	1	US-08-889-711-4	Sequence	4, Appli
42	40	50.6	428	2	US-09-185-825-4	Sequence	4, Appli
43	40	50.6	763	1	US-08-889-711-2	-	2, Appli
44	40	50.6	763	2	US-09-185-825-2	_	2, Appli
45	40	50.6	763	2	US-09-583-110-3773	-	3773, Ap
46	40	50.6	776	2	US-09-107-433-3635		3635, Ap
47	39	49.4	312	2	US-09-538-092-256	Sequence	256, App
48	39	49.4	319	2	US-09-248-796A-18323	Sequence	18323, A
49	39	49.4	323	2	US-09-538-092-1093	Seguence	1093, Ap
50	39	49.4	327	2	US-09-538-092-1095		1095, Ap
51	39	49.4	327	2	US-09-949-016-6266		6266, Ap
52	39	49.4	330	2	US-09-167-206-6	_	6, Appli
53	39	49.4	330	2	US-09-538-092-873	Sequence	873, App
54	39	49.4	330	2	US-09-190-976B-8	Sequence	8, Appli
55	39	49.4	356	2	US-09-949-016-8084	Sequence	8084, Ap
56	39	49.4	374	2	US-09-949-016-7363		7363, Ap
57	39	49.4	431	2	US-09-248-796A-16312		16312, A
58	39	49.4	685	2	US-10-094-749-2360		2360, Ap
59	38	48.1	49	2	US-09-270-767-33329	-	33329, A
60	38	48.1	49	2	US-09-270-767-48546	Sequence	48546, A
61	38	48.1	78	1	US-08-117-952-752	Sequence	752, App
62	38	48.1	106	2	US-09-746-801A-49		49, Appl
63	38	48.1	106	2	US-10-719-885-49		49, Appl
03	50	40.1	100	_	00 10 115 000-45	Dequence	10, What

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:29:53; Search time 75.9934 Seconds

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-26

Perfect score: 79

Sequence: 1 GRLIIEFKVNFPENG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA Main:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용 Result Query No. Score Match Length DB ID Description 79 100.0 15 4 US-10-001-938-26 Sequence 26, Appl

				_			
2	79	100.0	258	5	US-10-473-127-1141	Sequence	1141, Ap
3	79	100.0	258	5	US-10-473-127-1146	Sequence	1146, Ap
4	79	100.0	397	3	US-09-919-039-178		178, App
5	79	100.0	397	5	US-10-473-127-1138	-	1138, Ap
6	79		397	5	US-10-473-127-1139		
		100.0		_			1139, Ap
7	79	100.0	397	5	US-10-473-127-1140	_	1140, Ap
8	79	100.0	397	5	US-10-473-127-1143	Sequence	1143, Ap
9	79	100.0	397	5	US-10-473-127-1144	Sequence	1144, Ap
10	79	100.0	397	5	US-10-473-127-1145		1145, Ap
11	79	100.0	397	5	US-10-756-149-4727	_	4727, Ap
12	79	100.0	397	5	US-10-631-467-559	_	
							559, App
13	79	100.0	397	5	US-10-631-467-1386		1386, Ap
14	79	100.0	397	5	US-10-878-556A-155	Sequence	155, App
15	79	100.0	408	5	US-10-450-763-40099	Sequence	40099, A
16	6 7	84.8	291	5	US-10-450-763-40097	Sequence	40097, A
17	58	73.4	204	4	US-10-767-701-39910	_	39910, A
18	58	73.4	416	4	US-10-437-963-188385	Sequence	
19	55		420	4	US-10-437-963-128712		
		69.6				Sequence	
20	55	69.6	420	4	US-10-767-701-46164	_	46164, A
21	55	69.6	433	4	US-10-425-114-63266	Sequence	63266, A
22	55	69.6	435	4	US-10-425-114-59462	Sequence	59462, A
23	53	67.1	398	4	US-10-425-114-55344	_	55344, A
24	53	67.1	420	4	US-10-424-599-257607	Sequence	
25	53	67.1	420	4	US-10-424-599-257608	-	
				-		Sequence	
26	53	67.1	424	4	US-10-425-114-46242	_	46242, A
27	52	65.8	422	4	US-10-425-115-332061	Sequence	332061,
28	52	65.8	435	4	US-10-425-114-65366	Sequence	65366, A
29	50	63.3	348	5	US-10-871-388-1	Sequence	1, Appli
30	48	60.8	104	4	US-10-425-115-237886	Sequence	
31	48	60.8	455	4	US-10-369-493-12873	-	12873, A
32	47	59.5	58	4	US-10-424-599-163018	-	
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33	47	59.5	340	4	US-10-116-275-134		134, App
34	47	59.5	340	4	US-10-116-275-135		135, App
35	47	59.5	340	5	US-10-871-388-5	Sequence	5, Appli
36	47	59.5	340	5	US-10-792-571-16	Sequence	16, Appl
37	47	59.5	340	6	US-11-047-063-2		2, Appli
38	47	59.5	345	4	US-10-424-599-275932	Sequence	
39	47	59.5	349	5	US-10-732-923-18380	-	18380, A
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40	47	59.5	377	5	US-10-450-763-48884		48884, A
41	46	58.2	334	4	US-10-429-223-3		3, Appli
42	46	58.2	337	4	US-10-788-792-162		162, App
43	45	57.0	77	4	US-10-106-698-5915	Sequence	5915, Ap
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45	45	57.0	403	6	US-11-097-143-24405		24405, A
46	45	57.0	403	6	US-11-097-143-41904	-	41904, A
47						-	
	45	57.0	412	5	US-10-965-898-18		18, Appl
48	45	57.0	479	4	US-10-788-792-186		186, App
49	43	54.4	91	4	US-10-425-115-212526	Sequence	212526,
50	43	54.4	104	4	US-10-425-115-314381	Sequence	314381,
51	43	54.4	392	5	US-10-467-657-1784	Sequence	1784, Ap
52	43	54.4	439	4	US-10-369-493-6325	_	6325, Ap
53	43	54.4	666	4	US-10-724-972A-7129	-	7129, Ap
54	42	53.2	90	4	US-10-425-115-189463	-	_
						Sequence	
55	42	53.2	129	4	US-10-425-115-307676	Sequence	
56	42	53.2	136	4	US-10-767-701-47402	-	47402, A
57	42	53.2	174	4	US-10-425-115-314374	Sequence	
58	42	53.2	205	6	US-11-096-568A-21365	Sequence	21365, A
59	42	53.2	206	6	US-11-096-568A-15004		15004, A
60	42	53.2	210	4	US-10-425-115-209770	Sequence	
61	42	53.2	228	4	US-10-767-701-46318	-	46318, A
62	42			-			
02	42	53.2	228	4	US-10-425-115-314380	Sequence	314300,

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

US-10-001-938-26 Title:

Perfect score: 79

1 GRLIIEFKVNFPENG 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

> 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
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2	53	67.1	338	6	US-10-953-349-13711	Sequence 13711, A
3	53	67.1	382	6	US-10-953-349-13710	Sequence 13710, A
4	53	67.1	420	6	US-10-953-349-13709	Sequence 13709, A
5	43	54.4	257	6	US-10-953-349-1056	Sequence 1056, Ap
6	43	54.4	337	6	US-10-953-349-1055	Sequence 1055, Ap
7	43	54.4	419	6	US-10-953-349-1054	Sequence 1054, Ap
8	41	51.9	87	6	US-10-953-349-38753	Sequence 38753, A
9	41	51.9	93	6	US-10-953-349-38752	Sequence 38752, A
10	41	51.9	95	6	US-10-953-349-38751	Sequence 38751, A
11	40	50.6	256	6	US-10-953-349-16379	Sequence 16379, A
12	40	50.6	316	6	US-10-953-349-36080	Sequence 36080, A
13	40	50.6	317	6	US-10-953-349-36079	Sequence 36079, A
14	40	50.6	336	6	US-10-953-349-16378	Sequence 16378, A
15	40	50.6	397	7	US-11-293-697-3837	Sequence 3837, Ap
16	40	50.6	417	6	US-10-953-349-16377	Sequence 16377, A
17	40	50.6	426	7	US-11-293-697-4751	Sequence 4751, Ap
18	40	50.6	763	7	US-11-122-986-338	Sequence 338, App
19	40	50.6	763	7	US-11-122-986-340	Sequence 340, App
20	39	49.4	278	6	US-10-953-349-2767	Sequence 2767, Ap
21	39	49.4	304	6	US-10-953-349-2766	Sequence 2766, Ap
22	39	49.4	312	6	US-10-953-349-2765	Sequence 2765, Ap
23	38	48.1	158	6	US-10-953-349-39181	Sequence 39181, A
24	38	48.1	175	6	US-10-953-349-39180	Sequence 39180, A
25	38	48.1	187	6	US-10-953-349-39179	Sequence 39179, A
26	38	48.1	643	6	US-10-504-120-19	Sequence 19, Appl
27	38	48.1	1151	7	US-11-246-999-103	Sequence 103, App
28	38	48.1	1366	6	US-10-985-570-3	Sequence 3, Appli
29	36	45.6	189	6	US-10-953-349-9120	Sequence 9120, Ap
30	36	45.6	192	6	US-10-953-349-9119	Sequence 9119, Ap
31	36	45.6	248	6	US-10-953-349-9118	Sequence 9118, Ap
32	36	45.6	523	6	US-10-953-349-36009	Sequence 36009, A
33	36	45.6	565	6	US-10-953-349-36008	Sequence 36008, A
34	36	45.6	2209	7	US-11-301-554-1903	Sequence 1903, Ap
35	35	44.3	213	6	US-10-953-349-19718	Sequence 19718, A
36	35	44.3	250	6	US-10-953-349-19717	Sequence 19717, A
37	35	44.3	392	6	US-10-953-349-5472	Sequence 5472, Ap
38	35	44.3	511	7	US-11-121-154-96	Sequence 96, Appl
39		43.0		6		Sequence 39676, A
40	34	43.0	153	7	US-11-244-348A-6	Sequence 6, Appli
41	34	43.0	243	6	US-10-953-349-39675	Sequence 39675, A
42	34	43.0	308	6	US-10-953-349-19157	Sequence 19157, A
43	34	43.0	334	6	US-10-953-349-9073	Sequence 9073, Ap
44	34	43.0	348	6	US-10-953-349-14087	Sequence 14087, A
45	34	43.0	369	6	US-10-953-349-14086	Sequence 14086, A
46	34	43.0	385	6	US-10-953-349-9072	Sequence 9072, Ap
47	34	43.0	390	6	US-10-953-349-9071	Sequence 9071, Ap
48	34	43.0	458	6	US-10-196-749-498	Sequence 498, App
49	34	43.0	464	6	US-10-505-928-757	Sequence 757, App
50	34	43.0	466	6	US-10-953-349-22705	Sequence 22705, A
51 52	34	43.0	483	6	US-10-953-349-22704	Sequence 22704, A
52 53	34	43.0	516 524	6	US-10-953-349-23783	Sequence 23783, A
53 54	34 34	43.0	534 551	6	US-10-953-349-22703	Sequence 22703, A
54 55	34 34	43.0 43.0	551 592	7 6	US-11-236-238-29	Sequence 29, Appl
56	34	43.0	592 596	6	US-10-953-349-23782 US-10-953-349-23781	Sequence 23782, A
57	34	43.0	644	7	US-11-244-348A-5	Sequence 23781, A Sequence 5, Appli
5 <i>7</i>	34	43.0	1025	6	US-11-244-346A-5 US-10-505-928-505	Sequence 505, Appli
59	33.5	42.4	230	7	US-11-118-112A-220	Sequence 220, App
55	33.3	-16.7	230	′	00 II II0 II2A 220	bequeitee 220, App

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-3.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 3.rai.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:37:25; Search time 15.5789 Seconds

(without alignments)

89.896 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1 2	86 86	100.0	131 131	_	US-09-553-498-4 US-09-618-869-4	Sequence 4, Appli Sequence 4, Appli

_				•	540 6017 5010	- 5010 7
3	86	100.0	380	2	US-09-543-681A-5912	Sequence 5912, Ap
4	86	100.0	380	2	US-09-489-039A-9011	Sequence 9011, Ap
5	86	100.0	399	2	US-09-553-498-2	Sequence 2, Appli
6	86	100.0	399	2	US-09-618-869-2	Sequence 2, Appli
7	81	94.2	15	1	US-08-618-464-4	Sequence 4, Appli
8	81	94.2	15	2	US-09-107-615-4	Sequence 4, Appli
9	81	94.2	15	2	US-09-756-983-10	Sequence 10, Appl
10	81	94.2	15	2	US-10-299-184A-4	Sequence 4, Appli
11	81	94.2	15	2	US-09-828-574A-10	Sequence 10, Appl
12	81	94.2	15	3	US-09-421-506-10	Sequence 10, Appl
13	81	94.2	15	5	PCT-US95-04896-4	Sequence 4, Appli
14	72	83.7	15	1	US-08-618-464-5	Sequence 5, Appli
15	72	83.7	15	2	US-09-107-615-5	Sequence 5, Appli
16	72	83.7	15	2	US-10-299-184A-5	Sequence 5, Appli
17	72	83.7	15	2	US-09-828-574A-11	
						Sequence 11, Appl
18	72	83.7	15	5	PCT-US95-04896-5	Sequence 5, Appli
19	67	77.9	376	3	US-10-375-010-22	Sequence 22, Appl
20	62	72.1	381	2	US-09-252-991A-27174	Sequence 27174, A
21	61	70.9	407	2	US-09-540-236-2899	Sequence 2899, Ap
22	60	69.8	368	2	US-09-861-451A-2	Sequence 2, Appli
23	56	65.1	352	1	US-08-472-534-6	Sequence 6, Appli
24	56	65.1	378	2	US-09-583-110-4647	Sequence 4647, Ap
25	56	65.1	379	2	US-09-107-433-3487	Sequence 3487, Ap
26	54	62.8	15	1	US-08-618-464-6	Sequence 6, Appli
27	54	62.8	15	2	US-09-107-615-6	Sequence 6, Appli
28	54	62.8	15	2	US-10-299-184A-6	Sequence 6, Appli
29	53	61.6	240	2	US-09-248-796A-17703	Sequence 17703, A
30	52	60.5	375	2	US-09-328-352-4984	-
31	47	54.7	138	2		Sequence 4984, Ap
					US-09-902-540-13689	Sequence 13689, A
32	47	54.7	373	2	US-09-710-279-890	Sequence 890, App
33	47	54.7	385	2	US-09-134-001C-3688	Sequence 3688, Ap
34	47	54.7	595	2	US-10-104-047-2714	Sequence 2714, Ap
35	46	53.5	419	1	US-08-686-417-3	Sequence 3, Appli
36	45	52.3	677	2	US-09-252-991A-18102	Sequence 18102, A
37	44	51.2	387	2	US-09-908-992B-11	Sequence 11, Appl
38	44	51.2	397	2	US-09-248-796A-17628	Sequence 17628, A
39	44	51.2	414	2	US-09-908-992B-10	Sequence 10, Appl
40	44	51.2	452	2	US-09-908-992B-29	Sequence 29, Appl
41	44	51.2	453	2	US-09-908-992B-9	Sequence 9, Appli
42	44	51.2	453	2	US-09-908-992B-30	Sequence 30, Appl
43	44	51.2	479	2	US-09-908-992B-28	Sequence 28, Appl
44	44	51.2	480	2	US-09-908-992B-8	Sequence 8, Appli
45	44	51.2	480	2	US-09-908-992B-12	Sequence 12, Appl
46	44	51.2	915	2	US-09-252-991A-24992	Sequence 24992, A
47	43	50.0	1895	1	US-08-619-554-4	Sequence 4, Appli
48	43	50.0	1895	2	US-09-487-558B-136	Sequence 136, App
49	41	47.7	87	2	US-09-882-835-4	Sequence 4, Appli
50	41			2	US-10-094-749-2011	
		47.7	191			Sequence 2011, Ap
51	41	47.7	223	2	US-09-658-644-4	Sequence 4, Appli
52	41	47.7	223	2	US-09-949-016-6832	Sequence 6832, Ap
53	41	47.7	267	2	US-09-949-016-11497	Sequence 11497, A
54	41	47.7	348	1	US-08-974-546-1	Sequence 1, Appli
55	41	47.7	387	2	US-09-543-681A-7130	Sequence 7130, Ap
56	41	47.7	845	2	US-09-252-991A-29230	Sequence 29230, A
57	40	46.5	231	2	US-09-902-540-14837	Sequence 14837, A
58	40	46.5	317	2	US-09-328-352-8169	Sequence 8169, Ap
59	40	46.5	487	2	US-09-252-991A-21980	Sequence 21980, A
60	39	45.3	53	3	US-10-016-768A-2	Sequence 2, Appli
61	39	45.3	116	2	US-09-248-796A-21361	Sequence 21361, A
62	39	45.3	213	2	US-10-094-749-1949	Sequence 1949, Ap
63	39	45.3	442	3	US-10-016-768A-8	Sequence 8, Appli

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-3.ra

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 3.rapbm.

<u>start</u>

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:58:51; Search time 67.5789 Seconds

(without alignments)

109.671 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description		
1		100.0		 4 3	US-10-001-938-3 US-09-764-868-1153	Sequence 3, Appli Sequence 1153, Ap		
3		100.0		_	US-09-764-868-1153 US-09-764-868-1152	Sequence 1153, Ap		

4	86	100.0	376	4	US-10-369-493-689	Sequence 6	20 700
5	86	100.0	376	-	US-11-080-458-32	-	
				6		Sequence 3	
6	86	100.0	378	4	US-10-369-493-386	Sequence 3	
7	86	100.0	378	4	US-10-369-493-21305	Sequence 2	
8	86	100.0	476	5	US-10-450-763-48130	Sequence 4	8130, A
. 9	81	94.2	15	3	US-09-756-983-10	Sequence 1	0, Appl
10	81	94.2	15	3	US-09-828-574-10	Sequence 1	0, Appl
11	81	94.2	15	4	US-10-001-938-27	Sequence 2	7, Appl
12	81	94.2	15	4	US-10-299-540-4	Sequence 4	
13	81	94.2	15	4	US-10-299-184-4	Sequence 4	
14	81	94.2	15	4	US-10-239-313A-444	Sequence 4	
15	81	94.2	15	5	US-10-614-639A-10	-	
		94.2				Sequence 1	
16	81		15	5	US-10-614-414A-10	Sequence 1	
17	81	94.2	15	5	US-10-960-855-10	Sequence 1	
18	81	94.2	15	6	US-11-080-458-10	Sequence 1	
19	81	94.2	16	4	US-10-239-313A-447	Sequence 4	47, App
20	79	91.9	365	4	US-10-369-493-10648	Sequence 1	0648, A
21	78	90.7	376	4	US-10-369-493-12087	Sequence 1:	2087, A
22	73	84.9	344	5	US-10-467-657-8284	Sequence 82	
23	72	83.7	15	3	US-09-828-574-11	Sequence 1:	_
24	72	83.7	15	4	US-10-299-540-5	Sequence 5	
25	72	83.7	15	4	US-10-299-184-5	Sequence 5	
26	72	83.7	15	6		-	
					US-11-080-458-11	Sequence 1	
27	69	80.2	382	4	US-10-369-493-8065	Sequence 8	_
28	69	80.2	384	4	US-10-369-493-21849	Sequence 2	
29	67	77.9	376	4	US-10-375-010-22	Sequence 2	2, Appl
30	67	77.9	376	6	US-11-232-406A-22	Sequence 2	2, Appl
31	67	77.9	379	4	US-10-369-493-7330	Sequence 7:	330, Ap
32	67	77.9	380	4	US-10-369-493-4573	Sequence 4	573, Ap
33	63	73.3	376	4	US-10-369-493-47	Sequence 4	_
34	62	72.1	374	4	US-10-369-493-13658	Sequence 1	
35	61	70.9	378	4	US-10-369-493-8450	Sequence 8	
36	61	70.9	385	5	US-10-501-282-4398	Sequence 4:	
37	60	69.8	368	3	US-09-861-451A-2	Sequence 2	
38	60	69.8	375	4	US-10-369-493-15859		
				_		Sequence 1	
39	60 50	69.8	376	4	US-10-369-493-15487	Sequence 1	
40	59	68.6	358	4	US-10-369-493-9641	Sequence 9	_
41	58	67.4	379	4	US-10-369-493-18523	Sequence 1	
42	58	67.4	385	4	US-10-369-493-16754	Sequence 1	6754, A
43	57	66.3	369	4	US-10-369-493-19646	Sequence 1	9646, A
44	57	66.3	377	6	US-11-045-004-1504	Sequence 1	504, Ap
45	56	65.1	362	4	US-10-369-493-9305	Sequence 9:	305, Ap
46	56	65.1	378	4	US-10-474-776-634	Sequence 6	34, App
47	56	65.1	378	5	US-10-472-928-900	Sequence 9	
48	56	65.1	379	5	US-10-617-320-3487	Sequence 3	
49	54	62.8	15	4	US-10-299-540-6	Sequence 6	_
50	54	62.8	15	4	US-10-299-184-6	Sequence 6	
51	54	62.8	318	4	US-10-425-115-239397		
52				_		Sequence 23	
	53	61.6	423	4	US-10-369-493-12619	Sequence 1	
53	52	60.5	360	4	US-10-369-493-10371	Sequence 1	
54	52	60.5	372	4	US-10-369-493-23206	Sequence 2:	
55	52	60.5	376	4	US-10-369-493-1212	Sequence 1:	_
56	52	60.5	395	6	US-11-079-463-9803	Sequence 9	803, Ap
57	50	58.1	175	4	US-10-767-701-40315	Sequence 4	0315, A
58	50	58.1	241	4	US-10-425-115-289174	Sequence 2	89174,
59	50	58.1	297	4	US-10-282-122A-54551	Sequence 5	
60	50	58.1	334	6	US-11-096-568A-24300	Sequence 2	
61	50	58.1	362	4	US-10-437-963-190831	Sequence 1	
62	50	58.1	362	4	US-10-425-115-289176	Sequence 2	
63	50	58.1	362	6	US-11-096-568A-24299	Sequence 2	
64	50	58.1	383	4	US-10-437-963-108162	_	
0 4	50	50.1	505	7	02 10-427-202-100102	Sequence 1	00102,

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-3.rapbn.

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SCORE FAQ

Comments / Suggestions

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:45:07; Search time 3.78947 Seconds

(without alignments)

48.831 Million cell updates/sec

US-10-001-938-3 Title:

Perfect score: 86

Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 segs, 11565156 residues

58871 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description
1	86	100.0	16	6	US-10-490-949-4	Sequence 4, Appli
2	81	94.2	15	6	US-10-490-949-10	Sequence 10, Appl
3	72	83.7	15	6	US-10-490-949-11	Sequence 11, Appl
4	63	73.3	389	7	US-11-122-986-185	Sequence 185, App
5	63	73.3	389	7	US-11-122-986-187	Sequence 187, App
6	59	68.6	332	6	US-10-953-349-1407	Sequence 1407, Ap
7	59	68.6	367	6	US-10-953-349-1406	Sequence 1406, Ap
8	59	68.6	456	6	US-10-953-349-1405	Sequence 1405, Ap
9	54	62.8	15	6	US-10-490-949-1	Sequence 1, Appli
10	49	57.0	307	6	US-10-953-349-2183	Sequence 2183, Ap
11	49	57.0	335	6	US-10-953-349-2182	Sequence 2182, Ap
12	49	57.0	343	6	US-10-953-349-2181	Sequence 2181, Ap
13 14	48 46	55.8	141	6 6	US-10-953-349-10348	Sequence 10348, A
15	46	53.5 53.5	186 419	6	US-10-953-349-16110 US-10-953-349-1054	Sequence 16110, A Sequence 1054, Ap
16	43	50.0	308	6	US-10-953-349-1054 US-10-953-349-33811	Sequence 33811, A
17	43	50.0	336	6	US-10-953-349-33810	Sequence 33810, A
18	43	50.0	430	6	US-10-953-349-33809	Sequence 33809, A
19	42	48.8	339	6	US-10-953-349-12422	Sequence 12422, A
20	42	48.8	382	6	US-10-953-349-13710	Sequence 13710, A
21	42	48.8	420	6	US-10-953-349-13709	Sequence 13709, A
22	41	47.7	321	6	US-10-953-349-950	Sequence 950, App
23	41	47.7	323	6	US-10-953-349-949	Sequence 949, App
24	41	47.7	346	6	US-10-953-349-4235	Sequence 4235, Ap
25	41	47.7	349	6	US-10-953-349-948	Sequence 948, App
26	41	47.7	363	6	US-10-953-349-4234	Sequence 4234, Ap
27	41	47.7	380	6	US-10-953-349-7175	Sequence 7175, Ap
28	41	47.7	381	6	US-10-953-349-4233	Sequence 4233, Ap
29	41	47.7	391	6	US-10-953-349-7174	Sequence 7174, Ap
30	41	47.7	442	6	US-10-953-349-7173	Sequence 7173, Ap
31	40	46.5	417	6	US-10-953-349-16377	Sequence 16377, A
32	39	45.3	1386	7	US-11-314-018-6	Sequence 6, Appli
33 34	38 38	44.2 44.2	166 221	6 6	US-10-953-349-16554 US-10-953-349-16553	Sequence 16554, A Sequence 16553, A
35	38	44.2	231	6	US-10-953-349-16552	Sequence 16552, A
36	36	41.9	74	6	US-10-953-349-14225	Sequence 14225, A
37	36	41.9	96	6	US-10-953-349-14224	Sequence 14224, A
38	36	41.9	270	6	US-10-953-349-29919	Sequence 29919, A
39		41.9		6		Sequence 29918, A
40	36	41.9	341	6	US-10-953-349-29917	Sequence 29917, A
41	36	41.9	397	7	US-11-293-697-3837	Sequence 3837, Ap
42	36	41.9	426	7	US-11-293-697-4751	Sequence 4751, Ap
43	35	40.7	179	6	US-10-953-349-7415	Sequence 7415, Ap
44	35	40.7	189	6	US-10-953-349-9120	Sequence 9120, Ap
45	35	40.7	189	7	US-11-293-697-4556	Sequence 4556, Ap
46	35	40.7	192	6	US-10-953-349-9119	Sequence 9119, Ap
47	35	40.7	230	6	US-10-953-349-7414	Sequence 7414, Ap
48	35	40.7	248	6	US-10-953-349-9118	Sequence 9118, Ap
49	35	40.7	271	6	US-10-953-349-18081	Sequence 18081, A
50 51	35 35	40.7 40.7	273 314	6 6	US-10-953-349-18080 US-10-953-349-18079	Sequence 18080, A Sequence 18079, A
52	35	40.7		6	US-10-953-349-18079	Sequence 2047, Ap
53	35	40.7		6	US-10-953-349-2047 US-10-953-349-2046	Sequence 2046, Ap
54	35	40.7	731	7	US-11-293-697-3006	Sequence 3006, Ap
55	34	39.5	15	6	US-10-490-949-16	Sequence 16, Appl
56	34	39.5	15	6	US-10-490-949-17	Sequence 17, Appl
57	34	39.5	89	6	US-10-953-349-36746	Sequence 36746, A
58	34	39.5	174	6	US-10-953-349-15236	Sequence 15236, A
59	34	39.5	211	6	US-10-953-349-27572	Sequence 27572, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-4.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 4.rai.

<u>start</u>

Go Back to p

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OM protein - protein search, using sw model

June 2, 2006, 19:08:52; Search time 11.4238 Seconds Run on:

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-4

Perfect score: 90

Sequence: 1 QGFFAVQQTCPHCQG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description	
1	90 90	100.0	380 399		US-09-489-039A-9011 US-09-553-498-2	Sequence 9011, Ap Sequence 2, Appli	

_				_			
3	90	100.0	399	2	US-09-618-869-2	Sequence	2, Appli
4	74	82.2	381	2	US-09-252-991A-27174	Sequence	27174, A
5	73	81.1	376	3	US-10-375-010-22	Sequence	22, Appl
6	69	76.7	407	2	US-09-540-236-2899	Sequence	2899, Ap
7	65	72.2	380	2	US-09-543-681A-5912	_	5912, Ap
8	64	71.1	375	2	US-09-328-352-4984	_	4984, Ap
9	54	60.0	392	2	US-09-198-452A-48	-	_
							48, Appl
10	54	60.0	406	2	US-09-438-185A-34		34, Appl
11	50	55.6	209	2	US-09-902-540-14118	•	14118, A
12	45	50.0	858	2	US-09-960-428-7	-	7, Appli
13	44	48.9	108	2	US-09-328-352-5857	Sequence	5857, Ap
14	44	48.9	125	2	US-09-328-352-7243	Sequence	7243, Ap
15	44	48.9	132	2	US-09-513-999C-6410	Sequence	6410, Ap
16	44	48.9	354	2	US-09-583-110-4854	_	4854, Ap
17	44	48.9	364	2	US-09-107-433-4701	_	4701, Ap
18	44	48.9	635	2	US-10-104-047-2128	-	2128, Ap
19	44	48.9	1007	2	US-09-252-991A-28773	=	_
						-	28773, A
20	43	47.8	110	2	US-08-858-207A-273		273, App
21	43	47.8	115	2	US-09-583-110-3398		3398, Ap
22	43	47.8	120	2	US-09-107-433-3440	Sequence	3440, Ap
23	43	47.8	296	2	US-09-270-767-57017	Sequence	57017, A
24	43	47.8	369	2	US-09-270-767-41773	Sequence	41773, A
25	43	47.8	505	2	US-09-489-039A-12262	Sequence	12262, A
26	42	46.7	350	2	US-09-252-991A-27255	_	27255, A
27	42	46.7	952	2	US-10-216-556A-2	_	2, Appli
28	41	45.6	119	2	US-09-598-747-2		2, Appli
29	41	45.6	186	2	US-09-248-796A-15844	-	15844, A
30	41	45.6	1404	2	US-09-345-473E-24	_	24, Appl
31	41	45.6	1404	2	US-09-862-027-24	_	
32	40	44.4	66	2		_	24, Appl
					US-09-248-796A-27118	_	27118, A
33	40	44.4	81	2	US-09-543-681A-6756		6756, Ap
34	40	44.4	118	2	US-09-621-976-4089		4089, Ap
35	40	44.4	288	2	US-09-949-016-7274	_	7274, Ap
36	40	44.4	288	2	US-09-964-899-21		21, Appl
37	40	44.4	373	2	US-09-710-279-890	Sequence	890, App
38	40	44.4	385	2	US-09-134-001C-3688	Sequence	3688, Ap
39	40	44.4	459	2	US-09-252-991A-32058	Sequence	32058, A
40	40	44.4	644	2	US-09-605-042A-38	Sequence	38, Appl
41	40	44.4	2789	2	US-09-949-016-8208	Sequence	8208, Ap
42	40	44.4	2871	2	US-09-538-092-1076	Sequence	1076, Ap
43	39	43.3	60	2	US-09-270-767-58063	_	58063, A
44	39	43.3	164	2	US-10-094-749-2758	_	2758, Ap
45	39	43.3	262	2	US-10-094-749-2390		2390, Ap
46	39	43.3	283	2	US-10-104-047-2687		2687, Ap
47	39	43.3	290	2	US-10-094-749-2565		2565, Ap
48						-	-
	39	43.3	303	2	US-09-248-796A-15837		15837, A
49	39	43.3	462	2	US-09-489-039A-12291		12291, A
50	39	43.3	508	2	US-09-134-001C-4570		4570, Ap
51	39	43.3	510	1	US-08-220-677A-2		2, Appli
52	39 .	43.3	512	2	US-09-107-532A-6559		6559, Ap
53	39	43.3	522	2	US-09-252-991A-28463		28463, A
54	39	43.3	523	2	US-09-328-352-6394	Sequence	6394, Ap
55	39	43.3	523	2	US-09-328-352-6395	Sequence	6395, Ap
56	39	43.3	524	2	US-09-540-236-2706	Sequence	2706, Ap
57	39	43.3	538	2	US-09-543-681A-4490	_	4490, Ap
58	39	43.3	545	2	US-09-019-095A-38		38, Appl
59	39	43.3	606	2	US-09-134-000C-4093	_	4093, Ap
60	39	43.3	614	2	US-09-949-016-8536	-	8536, Ap
61	39	43.3	640	2	US-09-605-042A-40		40, Appl
62	39	43.3	673	2	US-10-104-047-2774		2774, Ap
63	39	43.3	816	1	US-08-820-170A-37		37, Appl
	3,5		010	_	05 00 020 1/OR 3/	Sequence	o,, whit

SCORE Search Results Details for Application 10 Search Result us-10-001-938-4.rapbn

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suga

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 <u>start</u>

> GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:29:53; Search time 75.9934 Seconds

(without alignments)

91.432 Million cell updates/sec

US-10-001-938-4 Title:

Perfect score: 90

Sequence: 1 QGFFAVQQTCPHCQG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published_Applications_AA_Main:* Database :

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	90	100.0	15	4	US-10-001-938-4	Sequence 4, Appli
2	90	100.0	340	3	US-09-764-868-1153	Sequence 1153, Ap
3	90	100.0	341	3	US-09-764-868-1152	Sequence 1152, Ap
4	90	100.0	376	4	US-10-369-493-689	Sequence 689, App

_	0.0	100 0	276	_	11 000 450 00	a .	
5	90	100.0	376	6	US-11-080-458-32		32, Appl
6	90	100.0	832	5	US-10-450-763-59430	_	59430, A
7	78	86.7	369	4	US-10-369-493-19646	-	19646, A
8	74	82.2	374	4	US-10-369-493-13658	Sequence	13658, A
9	73	81.1	376	4	US-10-375-010-22	Sequence	22, Appl
10	73	81.1	376	6	US-11-232-406A-22		22, Appl
11	72	80.0	379	4	US-10-369-493-7330		7330, Ap
12	72	80.0	380	4	US-10-369-493-4573		4573, Ap
13	71	78.9	376	4	US-10-369-493-12087	-	12087, A
14	70	77.8	362	4			
				_	US-10-369-493-9305	-	9305, Ap
15	69	76.7	378	4	US-10-369-493-8450		8450, Ap
16	68	75.6	375	4	US-10-369-493-15859		15859, A
17	68	75.6	376	4	US-10-369-493-15487	-	15487, A
18	67	74.4	378	4	US-10-369-493-386	Sequence	386, App
19	67	74.4	378	4	US-10-369-493-21305	Sequence	21305, A
20	64	71.1	382	4	US-10-369-493-8065	Sequence	8065, Ap
21	61	67.8	385	4	US-10-369-493-16754	Sequence	16754, A
22	60	66.7	365	4	US-10-369-493-10648	_	10648, A
23	57	63.3	384	4	US-10-369-493-21849	-	21849, A
24	56	62.2	344	5	US-10-467-657-8284		8284, Ap
25	54	60.0	392	4	US-10-289-762-48	_	48, Appl
26	53	58.9	339	4	US-10-369-493-19527	_	19527, A
27	53	58.9	376	4	US-10-369-493-47	-	47, Appl
28	51	56.7	274	4	US-10-305-475-47	_	
				_			7665, Ap
29	51	56.7	275	4	US-10-335-977-7664	=	7664, Ap
30	51	56.7	369	3	US-09-895-913A-180	-	180, App
31	51	56.7	369	4	US-10-335-977-7666	_	7666, Ap
32	50	55.6	666	6	US-11-098-686-11016	-	11016, A
33	49	54.4	123	3	US-09-867-550-1492	=	1492, Ap
34	49	54.4	275	4	US-10-158-057-230		230, App
35	49	54.4	385	5	US-10-501-282-4398	Sequence	4398, Ap
36	47	52.2	97	4	US-10-437-963-199043	Sequence	199043,
37	47	52.2	140	4	US-10-424-599-151787	Sequence	151787,
38	47	52.2	198	5	US-10-204-921-70	Sequence	70, Appl
39	47	52.2	572	4	US-10-267-502-268	Sequence	268, App
40	46	51.1	107	4	US-10-453-468-4	Sequence	4, Appli
41	46	51.1	261	5	US-10-631-467-702		702, App
42	46	51.1	374	6	US-11-087-099-5695	_	5695, Ap
43	45	50.0	225	4	US-10-424-599-166583	Sequence	-
44	45	50.0	608	4	US-10-161-493-112		112, App
45	45	50.0	769	4		Sequence	
46	45						
		50.0	858	3	US-09-960-428-7		7, Appli
47	45	50.0	1437	5	US-10-684-141-44		44, Appl
48	45	50.0	1437	5	US-10-810-486-44		44, Appl
49	44	48.9	97	4	US-10-425-115-259098	Sequence	
50	44	48.9	101	4	US-10-282-122A-44927		44927, A
51	44	48.9	112	5	US-10-450-763-58103		58103, A
52	44	48.9	226	3	US-09-971-361-11		11, Appl
53	44	48.9	226	6	US-11-108-870-11		11, Appl
54	44	48.9	298	6	US-11-097-143-21180	Sequence	21180, A
55	44	48.9	354	5	US-10-472-928-60	Sequence	60, Appl
56	44	48.9	364	5	US-10-617-320-4701	Sequence	4701, Ap
57	44	48.9	511	4	US-10-369-493-21871	Sequence	21871, A
58	44	48.9	513	6	US-11-097-143-11568	Sequence	11568, A
59	44	48.9	635	4	US-10-104-047-2128		2128, Ap
60	44	48.9	635	6	US-11-072-512-2128	-	2128, Ap
61	44	48.9	660	4	US-10-282-122A-47186		47186, A
62	43	47.8	79	4	US-10-425-115-193883	Sequence	
63	43	47.8	89	4	US-10-425-115-351689	Sequence	
64	43	47.8	115	4	US-10-425-115-200172	Sequence	
65	43	47.8	115	5	US-10-472-928-3058	_	3058, Ap
	-1.5	47.0	113	J	02 10 1,2 320 3030	Dequence	Jood, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-4.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title:

US-10-001-938-4

Perfect score: 90

Sequence:

1 QGFFAVQQTCPHCQG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description
1	90	100.0	15	6	US-10-490-949-5	Sequence 5, Appli
2	42	46.7	361	6	US-10-953-349-17037	Sequence 17037, A
3	42	46.7	375	6	US-10-953-349-17036	Sequence 17036, A
4	41	45.6	232	6	US-10-953-349-17867	Sequence 17867, A
5	41	45.6	244	6	US-10-953-349-17866	Sequence 17866, A
6	40	44.4	332	6	US-10-953-349-1407	Sequence 1407, Ap
7	40	44.4	360	6	US-10-953-349-38192	Sequence 38192, A
8	40	44.4	367	6	US-10-953-349-1406	Sequence 1406, Ap
9	40	44.4	451	6	US-10-953-349-38191	Sequence 38191, A
10	40	44.4	456	6	US-10-953-349-1405	Sequence 1405, Ap
11	39.5	43.9	225	7	US-11-293-697-4687	Sequence 4687, Ap
12	39	43.3	26	1	US-09-949-925-296	Sequence 296, App
13	39	43.3	79	1	US-09-949-925-294	Sequence 294, App
14	39	43.3	255	1	US-09-949-925-297	Sequence 297, App
15	39	43.3	457	6	US-10-953-349-13696	Sequence 13696, A
16	39	43.3	552	6	US-10-953-349-13695	Sequence 13695, A
17	39	43.3	577	7	US-11-293-697-3485	Sequence 3485, Ap
18	39	43.3	578	6	US-10-953-349-13694	Sequence 13694, A
19	39	43.3	724	7	US-11-293-697-3263	Sequence 3263, Ap
20	39	43.3	836	6	US-10-509-131-35	Sequence 35, Appl
21	39	43.3	836		US-11-293-697 - 3700	Sequence 3700, Ap
22	38	42.2	236		US-10-933-854-24	Sequence 24, Appl
23	38	42.2	691	6	US-10-511-937-2995	Sequence 2995, Ap
24	38	42.2	706	7	US-11-293-697 - 3919	Sequence 3919, Ap
25	37	41.1	256	6	US-10-623-808-6	Sequence 6, Appli
26	37	41.1	286	6	US-10-953-349-16858	Sequence 16858, A
27	37	41.1	302	6	US-10-953-349-16857	Sequence 16857, A
28	37	41.1	308	6	US-10-953-349-16856	Sequence 16856, A
29	37	41.1	338	6	US-10-953-349-13711	Sequence 13711, A
30	37	41.1	339	6	US-10-953-349-19392	Sequence 19392, A
31	37	41.1	382	6	US-10-953-349-13710	Sequence 13710, A
32	37	41.1	420		US-10-953-349-13709	Sequence 13709, A
33	37	41.1	442	6	US-10-953-349-19391	Sequence 19391, A
34	36.5	40.6	97		US-10-953-349-16420	Sequence 16420, A
35	36.5	40.6	190		US-11-293-697-3234	Sequence 3234, Ap
36	36	40.0	84		US-11-328-747-5	Sequence 5, Appli
37	36	40.0	97		US-10-953-349-34432	Sequence 34432, A
38	36	40.0	211	-	US-10-953-349-38932	Sequence 38932, A
39	36		214		US-10-953-349-9238	Sequence 9238, Ap
40	36	40.0	215		US-10-953-349-9237	Sequence 9237, Ap
41	36	40.0	306		US-11-249-111-110	Sequence 110, App
42	36	40.0	318		US-10-953-349-12208	Sequence 12208, A
43	36	40.0	320		US-10-953-349-20561	Sequence 20561, A
44	36	40.0	324		US-10-953-349-12207	Sequence 12207, A
45	36	40.0	326		US-10-953-349-20560	Sequence 20560, A
46	36	40.0	362		US-11-293-697-2645	Sequence 2645, Ap
47	36	40.0	481		US-11-293-697-4458	Sequence 4458, Ap
48	36	40.0	549		US-11-293-697-4179	Sequence 4179, Ap
49	36	40.0	1912		US-10-511-937-2561	Sequence 2561, Ap
50	35.5	39.4	452		US-11-326-489-5	Sequence 5, Appli
51 52	35	38.9			US-11-311-555-6	Sequence 6, Appli
52	35	38.9			US-11-311-561-6	Sequence 6, Appli
53	35	38.9			US-11-101-316-156	Sequence 156, App
54 55	35	38.9			US-10-953-349-38933	Sequence 38933, A
55 56	35 35	38.9 38.9	253 350		US-10-953-349-19102 US-11-101-316-8	Sequence 19102, A Sequence 8, Appli
50 57	35	38.9			US-10-505-928-163	Sequence 163, App
5 <i>7</i> 58	35	38.9			US-10-953-349-427	Sequence 427, App
59	35	38.9	750 757		US-10-953-349-427	Sequence 427, App
3,5	33	50.9	,,,	U	00 10 000 010 120	bequeince 420, App

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-5.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 5.rai.

start

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OM protein - protein search, using sw model

June 2, 2006, 19:12:07; Search time 12.7 Seconds Run on:

(without alignments) 103.383 Million cell updates/sec

Title: US-10-001-938-5

Perfect score: 73

Sequence: 1 SKTLSVKIPGAVDTG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description	
1	63	86.3	399	2	US-09-553-498-2	Sequence 2, Appli	
2	63	86.3	399	2	US-09-618-869-2	Sequence 2, Appli	

_				_		_	
3	60	82.2	380	2	US-09-489-039A-9011		9011, Ap
4	59	80.8	380	2	US-09-543-681A-5912	Sequence	5912, Ap
5	58	79.5	381	2	US-09-252-991A-27174	Sequence	27174, A
6	51	69.9	376	3	US-10-375-010-22	Sequence	22, Appl
7	43	58.9	254	2	US-09-248-796A-17877	Sequence	17877, A
8	41	56.2	170	2	US-09-270-767-43106	_	43106, A
9	41	56.2	308	2	US-09-489-039A-8590		8590, Ap
10	41	56.2	320	2	US-09-543-681A-7884	_	7884, Ap
11	40	54.8	375	2	US-09-328-352-4984		4984, Ap
12				2		_	_
	40	54.8	407		US-09-540-236-2899	_	2899, Ap
13	39	53.4	62	2	US-09-489-039A-11677	-	11677, A
14	39	53.4	209	2	US-09-902-540-14118	_	14118, A
15	39	53.4	391	2	US-09-902-540-11110	Sequence	11110, A
16	39	53.4	595	2	US-09-248-796A-16455	Sequence	16455, A
17	38	52.1	206	2	US-09-270-767-32859	Sequence	32859, A
18	38	52.1	217	2	US-09-489-039A-7245	Sequence	7245, Ap
19	38	52.1	309	2	US-09-489-039A-10229	_	10229, A
20	38	52.1	352	1	US-08-472-534-6		6, Appli
21	38	52.1	364	1	US-08-570-311-26	_	26, Appl
22	38	52.1	378	2	US-09-583-110-4647	-	4647, Ap
23	38	52.1	379	2	US-09-107-433-3487		
						_	3487, Ap
24	38	52.1	905	2	US-09-248-796A-15706	=	15706, A
25	38	52.1	942	1	US-08-141-324-14	_	14, Appl
26	38	52.1	942	1	US-08-541-902-14	_	14, Appl
27	38	52.1	1732	1	US-08-570-311-10		10, Appl
28	38	52.1	1732	1	US-08-353-485-10	Sequence	10, Appl
29	38	52.1	1732	2	US-09-066-330-11	Sequence	11, Appl
30	37	50.7	233	1	US-08-221-750A-7	Sequence	7, Appli
31	37	50.7	266	2	US-09-252-991A-29750		29750, A
32	37	50.7	320	2	US-09-328-352-7937		7937, Ap
33	37	50.7	340	2	US-09-107-532A-7298	_	7298, Ap
34	37	50.7	395	2	US-09-712-363-164	-	164, App
35	37	50.7	493	2	US-09-613-303-19	-	19, Appl
36	37	50.7	493	2	US-10-267-311-19	_	
37	37					•	19, Appl
		50.7	606	2	US-09-248-796A-17830	_	17830, A
38	37	50.7	903	2	US-09-270-767-46470	=	46470, A
39	36.5	50.0	397	2	US-09-902-540-12830	-	12830, A
40	36	49.3	128	2	US-08-858-207A-314	=	314, App
41	36	49.3	154	2	US-09-248-796A-20059		20059, A
42	36	49.3	223	2	US-10-036-041-61	Sequence	61, Appl
43	36	49.3	227	2	US-09-208-718-3	Sequence	3, Appli
44	36	49.3	227	2	US-09-621-976-8	Sequence	8, Appli
45	36	49.3	227	2	US-09-513-999C-8	Sequence	8, Appli
46	36	49.3	227	2	US-09-471-276-8		8, Appli
47	36	49.3	273	2	US-09-198-452A-767	_	767, App
48	36	49.3	273	2	US-09-438-185A-723	_	723, App
49	36	49.3	360	2	US-09-543-681A-4783	-	4783, Ap
50	36	49.3	395	2	US-09-603-208A-28		28, Appl
51	36	49.3	485	2	US-09-902-540-9878		
52	36						9878, Ap
		49.3	664	2	US-09-489-039A-14017		14017, A
53	35	47.9	18	1	US-08-468-674B-8		8, Appli
54	35	47.9	18	1	US-08-780-571-8	-	8, Appli
55	35	47.9	18	2	US-09-324-217B-10		10, Appl
56	35	47.9	108	2	US-09-187-859-43	_	43, Appl
57	35	47.9	108	2	US-09-839-542B-43	Sequence	43, Appl
58	35	47.9	108	2	US-09-535-852-43	Sequence	43, Appl
59	35	47.9	108	2	US-10-006-869-43	Sequence	43, Appl
60	35	47.9	188	2	US-09-902-540-14832		14832, A
61	35	47.9	271	2	US-09-248-796A-16496	_	16496, A
62	35	47.9	310	2	US-09-614-912-202		202, App
63	35	47.9	344	2	US-09-489-039A-14341		14341, A
- •			911	_	12 03 103 00311 11011	Dequence	_ 10 11 / 17

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-5.ra

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 5.rapbm.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-5

Perfect score: 73

Sequence: 1 SKTLSVKIPGAVDTG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2097797 segs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

		8				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	73	100.0	15	4	US-10-001-938-5	Sequence 5, Appli
2	63	86.3	340	3	US-09-764-868-1153	Sequence 1153, Ap
3	63	86.3	341	3	US-09-764-868-1152	Sequence 1152, Ap

4	63	86.3	376	4	US-10-369-493-689	Sequence	689, App
5	63	86.3	376	6	US-11-080-458-32	Sequence	32, Appl
6	63	86.3	832	5	US-10-450-763-59430		59430, A
7	59	80.8	378	4	US-10-369-493-386		386, App
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8	59	80.8	378	4	US-10-369-493-21305	-	21305, A
9	58	79.5	374	4	US-10-369-493-13658	Sequence	13658, A
10	54	74.0	362	4	US-10-369-493-9305	Sequence	9305, Ap
11	52	71.2	375	4	US-10-369-493-15859	Sequence	15859, A
12	52	71.2	376	4	US-10-369-493-15487	_	15487, A
13	51	69.9	376	4	US-10-375-010-22		22, Appl
14	51	69.9	376	6	US-11-232-406A-22		22, Appl
				-		_	
15	50	68.5	288	4	US-10-369-493-8874	_	8874, Ap
16	50	68.5	369	4	US-10-369-493-19646	Sequence	19646, A
17	49	67.1	379	4	US-10-369-493-7330	Sequence	7330, Ap
18	49	67.1	380	4	US-10-369-493-4573	Sequence	4573, Ap
19	48	65.8	378	4	US-10-156-761-13102		13102, A
20	48	65.8	378	4	US-10-369-493-8450		8450, Ap
21	47	64.4	384	4	US-10-369-493-21849	-	21849, A
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22	47	64.4	461	4	US-10-424-599-254411	Sequence	
23	45	61.6	306	4	US-10-282-122A-73201		73201, A
24	45	61.6	306	4	US-10-282-122A-76109	Sequence	76109, A
25	45	61.6	343	5	US-10-972-024-277	Sequence	277, App
26	44	60.3	306	4	US-10-369-493-790		790, App
27	44	60.3	306	4	US-10-282-122A-42884		42884, A
28	44	60.3	374	4	US-10-424-599-253712	_	
				_		Sequence	
29	44	60.3	448	4	US-10-425-115-195339	Sequence	
30	44	60.3	478	4	US-10-425-114-65215		65215, A
31	43	58.9	305	4	US-10-369-493-13684	Sequence	13684, A
32	43	58.9	376	4	US-10-369-493-1212	Sequence	1212, Ap
33	43	58.9	382	4	US-10-369-493-8065	_	8065, Ap
34	42	57.5	319	4	US-10-282-122A-69287	_	69287, A
35	42	57.5	350	4	US-10-369-493-21024	_	21024, A
36	42	57.5	401	4		_	
				-	US-10-369-493-3465	-	3465, Ap
37	42	57.5	597	4	US-10-425-114-55831	_	55831, A
38	42	57.5	665	4	US-10-425-115-323605	Sequence	323605,
39	42	57.5	852	4	US-10-369-493-1645	Sequence	1645, Ap
40	41	56.2	53	4	US-10-016-157A-229	Sequence	229, App
41	41	56.2	53	6	US-11-042-241-229	-	229, App
42	41	56.2	147	4	US-10-425-115-267989	Sequence	
43	41	56.2	305	4	US-10-282-122A-59632	-	59632, A
44	41	56.2	314				69193, A
45	41	56.2	319	4	US-10-282-122A-68006		68006, A
46	41	56.2	385	4	US-10-369-493-16754	-	16754, A
47	41	56.2	423	4	US-10-369-493-12619	Sequence	12619, A
48	41	56.2	683	5	US-10-473-127-511	Sequence	511, App
49	41	56.2	683	5	US-10-473-127-512		512, App
50	41	56.2	683	5	US-10-473-127-513		513, App
51	41	56.2	683	5	US-10-473-127-514		514, App
52	41	56.2	683	5	US-10-473-127-515		515, App
53	41	56.2	683	5	US-10-473-127-516	-	516, App
54	41	56.2	683	6	US-11-009-554-9		9, Appli
55	41	56.2	905	4	US-10-451-467A-64	Sequence	64, Appl
56	41	56.2	913	6	US-11-097-143-4134	Sequence	4134, Ap
57	41	56.2	8943	5	US-10-745-237-190	Sequence	190, App
58	40	54.8	125	4	US-10-156-761-11979		11979, A
59	40	54.8	228	4	US-10-437-963-189989	Sequence	
60	40			_		_	
		54.8	296	4	US-10-282-122A-61258		61258, A
61	40	54.8	312	4	US-10-282-122A-50995		50995, A
62	40	54.8	344	5	US-10-467-657-8284		8284, Ap
63	40	54.8	674	4	US-10-369-493-12648		12648, A
64	39.5	54.1	751	3	US-09-795-693-14	Sequence	14, Appl
						_	

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-5.rapbn.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title: US-10-001-938-5

Perfect score: 73

1 SKTLSVKIPGAVDTG 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

> 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	73	100.0	15	6	US-10-490-949-6	Sequence 6, Appli
2	44	60.3	202	6	US-10-953-349-11146	Sequence 11146, A
3	44	60.3	219	6	US-10-953-349-11145	Sequence 11145, A
4	44	60.3	222	6	US-10-953-349-11144	Sequence 11144, A
5	44	60.3	380	6	US-10-953-349-7175	Sequence 7175, Ap
6	44	60.3	391	6	US-10-953-349-7174	Sequence 7174, Ap
7	44	60.3	442	6	US-10-953-349-7173	Sequence 7173, Ap
8	38	52.1	354	6	US-10-953-349-4966	Sequence 4966, Ap
9	38	52.1	432	6	US-10-953-349-4965	Sequence 4965, Ap
10	38	52.1	502	6	US-10-953-349-4964	Sequence 4964, Ap
11	35	47.9	371	6	US-10-953-349-10961	Sequence 10961, A
12	35	47.9	457	6	US-10-953-349-10960	Sequence 10960, A
13	35	47.9	490	6	US-10-953-349-10959	Sequence 10959, A
14	35	47.9	5738	6	US-10-505-928-150	Sequence 150, App
15	34	46.6	118	7	US-11-293-697-2755	Sequence 2755, Ap
16	34	46.6	209	6	US-10-953-349-29859	Sequence 29859, A
17	34	46.6	267	6	US-10-953-349-29858	Sequence 29858, A
18	34	46.6	293	6	US-10-953-349-29857	Sequence 29857, A
19	34	46.6	545	7	US-11-293-697-2487	Sequence 2487, Ap
20	33	45.2	188	6	US-10-953-349-16041	Sequence 16041, A
21	33	45.2	273	6	US-10-953-349-34506	Sequence 34506, A
22	33	45.2	285	6	US-10-953-349-13230	Sequence 13230, A
23	33	45.2	297	6	US-10-953-349-16040	Sequence 16040, A
24	33	45.2	300	6	US-10-953-349-16039	Sequence 16039, A
25 26	33 33	45.2 45.2	303	6 6	US-10-953-349-34505	Sequence 34505, A
26 27	33	45.2	315 319	6	US-10-953-349-4747	Sequence 4747, Ap
28	33	45.2	335	6	US-10-953-349-5745 US-10-953-349-13229	Sequence 5745, Ap Sequence 13229, A
29	33	45.2	341	6	US-10-953-349-13229	Sequence 5744, Ap
30	33	45.2	347	6	US-10-953-349-13228	Sequence 13228, A
31	33	45.2	391	6	US-10-953-349-5743	Sequence 5743, Ap
32	33	45.2	428	6	US-10-196-749-514	Sequence 514, App
33	33	45.2	436	6	US-10-953-349-4746	Sequence 4746, Ap
34	33	45.2	465	6	US-10-953-349-4745	Sequence 4745, Ap
35	33	45.2	534	7	US-11-121-154-135	Sequence 135, App
36	32	43.8	134	6	US-10-953-349-15674	Sequence 15674, A
37	32	43.8	154	6	US-10-953-349-13884	Sequence 13884, A
38	32	43.8	215	6	US-10-953-349-13402	Sequence 13402, A
39	32	43.8	260	6	US-10-953-349-13883	Sequence 13883, A
40	32	43.8	290	6	US-10-953-349-5422	Sequence 5422, Ap
41	32	43.8	298	7	US-11-293-697-2712	Sequence 2712, Ap
42	32	43.8	312	7	US-11-140-450-81	Sequence 81, Appl
43	32	43.8	320	6	US-10-953-349-16365	Sequence 16365, A
44	32	43.8	363	6	US-10-953-349-16364	Sequence 16364, A
45	32	43.8	384	6	US-10-953-349-16363	Sequence 16363, A
46	32	43.8	426	6	US-10-953-349-5421	Sequence 5421, Ap
47	32	43.8	513	6	US-10-953-349-32711	Sequence 32711, A
48	32	43.8	529	7	US-11-223-945-34	Sequence 34, Appl
49	32	43.8	531	6	US-10-953-349-5420	Sequence 5420, Ap
50	32	43.8	548	6	US-10-953-349-32710	Sequence 32710, A
51 52	32 32	43.8	576	6	US-10-953-349-32301	Sequence 32301, A
53	32	43.8	613	6 7	US-10-953-349-32709	Sequence 32709, A
54	32	43.8 43.8	648 648	7	US-11-024-544A-8 US-11-190-750-60	Sequence 8, Appli Sequence 60, Appl
55	32	43.8	648	7	US-11-190-730-60 US-11-264-784-77	Sequence 77, Appl
56	32	43.8	648	7	US-11-264-737-118	Sequence 118, App
57	32	43.8	689	6	US-10-953-349-32300	Sequence 32300, A
58	32	43.8	695	7	US-11-258-767-26	Sequence 26, Appl
59	32	43.8	745	6	US-10-953-349-32299	Sequence 32299, A
				•		andanas anns h

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-6.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-0(6.rai.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:12:07; Search time 12.7 Seconds

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-6

Perfect score: 80

Sequence: 1 GDLYVQVQVKQHPIF 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1 2	80 80	100.0	399 399	2 2	US-09-553-498-2 US-09-618-869-2	Sequence 2, Appli Sequence 2, Appli

_				_		_	
3	72	90.0	380	2	US-09-489-039A-9011	Sequence	9011, Ap
4	63	78.8	380	2	US-09-543-681A-5912	Sequence	5912, Ap
5	62	77.5	376	3		-	•
					US-10-375-010-22	_	22, Appl
6	62	77.5	381	2	US-09-252-991A-27174	Sequence	27174, A
7	61	76.2	209	2	US-09-902-540-14118		14118, A
8	59	73.8	407	2	US-09-540-236-2899	Sequence	2899, Ap
9	56	70.0	375	2	US-09-328-352-4984	Sequence	4984, Ap
10	56	70.0	392	2	US-09-198-452A-48	_	48, Appl
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11	56	70.0	406	2	US-09-438-185A-34		34, Appl
12	54	67.5	382	2	US-09-603-208A-40	Sequence	40, Appl
13	52	65.0	391	2	US-09-902-540-11110		11110, A
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14	46	57.5	121	2	US-09-717-321A-29	Sequence	29, Appl
15	46	57.5	320	2	US-09-543-681A-7884	Sequence	7884, Ap
16	46	57.5	358	1	US-08-868-288A-1	=	1, Appli
				_			
17	46	57.5	358	2	US-09-235-373-1	Sequence	1, Appli
18	46	57.5	358	2	US-09-388-993-1	Sequence	1, Appli
19	46	57.5	358	2	US-09-991-181-148		148, App
20	46	57.5	358	2	US-09-501-714-1		1, Appli
21	46	57.5	358	2	US-09-990-444-148	Sequence	148, App
22	46	57.5	358	2	US-09-997-333-148	_	148, App
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23	46	57.5	358	2	US-09-992-598-148	Sequence	148, App
24	46	57.5	358	2	US-09-989-735-148	Sequence	148, App
25	46	57.5	358	3	US-09-989-726-148		148, App
				_		_	
26	46	57.5	358	3	US-09-997-514-148		148, App
27	46	57.5	358	3	US-09-989-728-148	Sequence	148, App
28	46	57.5	358	3	US-09-997-349-148		148, App
29	46	57.5	358	3	US-09-997-653-148	Sequence	148, App
30	46	57.5	358	3	US-09-989-293A-148	Sequence	148, App
31	45	56.2	368	2	US-09-861-451A-2		2, Appli
32							
	45	56.2	395	2	US-09-603-208A-28	sequence	28, Appl
33	44	55.0	286	2	US-09-902-540-11710	Sequence	11710, A
34	44	55.0	308	2	US-09-489-039A-8590	_	8590, Ap
35	43	53.8	324	2			
					US-09-248-796A-15091	_	15091, A
36	43	53.8	395	2	US-09-712-363-164	Sequence	164, App
37	43	53.8	493	2	US-09-613-303-19	Sequence	19, Appl
38	43	53.8	493	2	US-10-267-311-19	_	
							19, Appl
39	41	51.2	286	2	US-09-902-540-11427	Sequence	11427, A
40	40.5	50.6	450	2	US-09-857-524B-8	Seguence	8, Appli
41	40	50.0	180	2	US-09-936-588-45		45, Appl
42	40	50.0	288	2	US-09-107-532A-7120		7120, Ap
43	40	50.0	320	2	US-09-328-352-7937	Seguence	7937, Ap
44	40	50.0	505	2	US-09-902-540-12326	-	12326, A
45	40	50.0	579	2	US-09-489-039A-12334	Sequence	12334, A
46	40	50.0	608	2	US-09-310-275-2	Sequence	2, Appli
47	40	50.0	608	2	US-09-082-077-5		5, Appli
						_	
48	40	50.0	608	2	US-09-925-637-70		70, Appl
49	39.5	49.4	680	2	US-09-248-796A-15089	Sequence	15089, A
50	39	48.8	65	2	US-09-910-009A-357		357, App
51							
	38.5	48.1	446	1	US-08-833-610-5	-	5, Appli
52	38.5	48.1	446	2	US-08-834-033A-15	Sequence	15, Appl
53	38.5	48.1	446	2	US-09-377-452-5		5, Appli
54	38.5			2	US-09-555-093-7		
		48.1	447			_	7, Appli
55	38.5	48.1	448	1	US-08-366-779-5	Sequence	5, Appli
56	38.5	48.1	448	1	US-08-789-936-5		5, Appli
57	38.5		448	2	US-08-934-254-5		
		48.1					5, Appli
58	38.5	48.1	448	2	US-09-685-775-5	Sequence	5, Appli
59	38.5	48.1	448	2	US-09-857-583B-15		15, Appl
60	38.5	48.1	448	2	US-09-857-524B-11		11, Appl
61	38	47.5	67	2	US-09-910-009A-271	_	271, App
62	38	47.5	129	2	US-09-621-976-4541	Sequence	4541, Ap
63	38	47.5	244	2	US-09-134-000C-4358		4358, Ap
	33	5		-	22 03 20. 0000 4000	Dequence	.000, 1.p

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-6.ra

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 6.rapbm.

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OM protein - protein search, using sw model

June 2, 2006, 19:45:16; Search time 63.4 Seconds Run on:

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-6

Perfect score: 80

1 GDLYVQVQVKQHPIF 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

2097797 seqs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA Main:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:*

> 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1 2 3	80 80 80	100.0 100.0 100.0	341	3	US-10-001-938-6 US-09-764-868-1152 US-10-369-493-689	Sequence 6, Appli Sequence 1152, Ap Sequence 689, App

				_	11 000 450 00	_	
4	80	100.0	376	6	US-11-080-458-32	Sequence	
5	74	92.5	340	3	US-09-764-868-1153	Sequence	
6	70	87.5	378	4	US-10-369-493-8450	Sequence	_
7	67	83.8	362	4	US-10-369-493-9305	Sequence	9305, Ap
8	65	81.2	161	5	US-10-450-763-55085	Sequence	55085, A
9	65	81.2	378	4	US-10-369-493-386	Sequence	386, App
10	65	81.2	378	4	US-10-369-493-21305	Sequence	
11	62	77.5	376	4	US-10-375-010-22	Sequence	
12	62	77.5	376	6	US-11-232-406A-22	Sequence	
13	61	76.2	379	4	US-10-369-493-7330	Sequence	
14	61	76.2		4		_	_
			380	_	US-10-369-493-4573	Sequence	_
15	60	75.0	364	4	US-10-369-493-134	Sequence	
16	59	73.8	375	4	US-10-369-493-15859	Sequence	
17	59	73.8	376	4	US-10-369-493-15487	Sequence	
18	58	72.5	296	4	US-10-282-122A-61258	Sequence	61258, A
19	56	70.0	392	4	US-10-289-762-48	Sequence	48, Appl
20	55	68.8	396	4	US-10-156-761-12020	Sequence	12020, A
21	54	67.5	330	4	US-10-369-493-19832	Sequence	19832, A
22	54	67.5	331	4	US-10-369-493-18770	Sequence	
23	54	67.5	376	4	US-10-369-493-1212	Sequence	
24	54	67.5	382	3	US-09-738-626-6012	Sequence	-
25	54	67.5	382	5	US-10-703-799B-40	Sequence	-
	53					•	
26		66.2	236	4	US-10-424-599-282285	Sequence	
27	53	66.2	367	4	US-10-369-493-8095	Sequence	
28	53	66.2	374	4	US-10-369-493-13658	Sequence	
29	53	66.2	376	4	US-10-369-493-47	Sequence	
30	53	66.2	384	4	US-10-369-493-21849	Sequence	21849, A
31	53	66.2	458	4	US-10-424-599-282290	Sequence	282290,
32	52	65.0	214	4	US-10-425-114-61777	Sequence	61777, A
33	52	65.0	239	6	US-11-096-568A-18418	Sequence	18418, A
34	52	65.0	266	6	US-11-096-568A-18417	Sequence	18417, A
35	52	65.0	344	5	US-10-467-657-8284	Sequence	
36	52	65.0	368	4	US-10-369-493-19421	Sequence	_
37	52	65.0	419	4	US-10-437-963-201815	Sequence	
38	52	65.0	429	4	US-10-425-115-209640	Sequence	
39	52		429	6	US-11-096-568A-18416	Sequence	
		65.0					
40	51	63.7	168	4	US-10-767-701-39210	Sequence	
41	51	63.7	307	4	US-10-369-493-2647	Sequence	
42	51	63.7	317	4	US-10-156-761-14768	Sequence	
43	51	63.7	369	4	US-10-369-493-19646	Sequence	
44	51	63.7	382	4	US-10-369-493-8065	Sequence	
45	51	63.7	442	4	US-10-437-963-196211	Sequence	196211,
46	50	62.5	308	4	US-10-369-493-19014	Sequence	19014, A
47	50	62.5	332	4	US-10-369-493-2834	Sequence	2834, Ap
48	49	61.3	312	4	US-10-282-122A-50995	Sequence	50995, A
49	49	61.3	418	4	US-10-425-115-271144	Sequence	
50	49	61.3	528	4	US-10-369-493-22651	Sequence	
51	48	60.0	350	4	US-10-369-493-21024	Sequence	
52	48	60.0	420	4	US-10-369-493-591	Sequence	
53	47	58.8	310	4	US-10-369-493-4694	Sequence	
						-	
54	47	58.8	322	4	US-10-369-493-20073	Sequence	
55	47	58.8	329	4	US-10-282-122A-49700	Sequence	
56	47	58.8	358	4	US-10-369-493-9641	Sequence	_
57	47	58.8	391	4	US-10-369-493-18560	Sequence	
58	46	57.5	61	4	US-10-424-599-255229	Sequence	
59	46	57.5	289	4	US-10-458-143-20	Sequence	
60	46	57.5	314	4	US-10-282-122A-69193	Sequence	69193, A
61	46	57.5	319	4	US-10-282-122A-69287	Sequence	69287, A
62	46	57.5	358	3	US-09-989-722-148	Sequence	
63	46	57.5	358	3	US-09-989-723-148	Sequence	
64	46	57.5	358	3	US-09-989-279-148	Sequence	
-			-			<u> </u>	

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-6.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds (without alignments)

55.960 Million cell updates/sec

Title: US-10-001-938-6

Perfect score: 80

Sequence: 1 GDLYVQVQVKQHPIF 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Published Applications AA New:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

> 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:*

> 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description
1	80	100.0	15	6	US-10-490-949-7	Sequence 7, Appli
2	51	63.7	332	6	US-10-953-349-1407	Sequence 1407, Ap
3	51	63.7	367	6	US-10-953-349-1406	Sequence 1406, Ap
4	51	63.7	456	6	US-10-953-349-1405	Sequence 1405, Ap
5	43	53.8	338	6	US-10-953-349-13711	Sequence 13711, A
6	43	53.8	367	6	US-10-953-349-9124	Sequence 9124, Ap
7	43	53.8	382	6	US-10-953-349-13710	Sequence 13710, A
8	43	53.8	396	6	US-10-953-349-9123	Sequence 9123, Ap
9	43	53.8	406	6	US-10-953-349-9122	Sequence 9122, Ap
10	43	53.8	420	6	US-10-953-349-13709	Sequence 13709, A
11	41	51.2	257	6	US-10-953-349-1056	Sequence 1056, Ap
12	41	51.2	337	6	US-10-953-349-1055	Sequence 1055, Ap
13	41	51.2	419	6	US-10-953-349-1054	Sequence 1054, Ap
14	39	48.8	256	6	US-10-953-349-16379	Sequence 16379, A
15	39	48.8	336	6	US-10-953-349-16378	Sequence 16378, A
16	39	48.8	360	6	US-10-953-349-20603	Sequence 20603, A
17	39	48.8	389	6	US-10-953-349-20602	Sequence 20602, A
18	39	48.8	390	6	US-10-953-349-20601	Sequence 20601, A
19	39	48.8	402	6	US-10-953-349-4763	Sequence 4763, Ap
20	39	48.8	411	6	US-10-953-349-4762	Sequence 4762, Ap
21	39	48.8	415	6	US-10-953-349-4761	Sequence 4762, Ap
22	39	48.8	417	6	US-10-953-349-16377	Sequence 16377, A
23	38.5	48.1	448	6	US-10-975-692-15	Sequence 15, Appl
24	38	47.5	389	7	US-11-122-986-185	Sequence 185, App
25	38	47.5	389	7	US-11-122-986-187	Sequence 187, App
26	38	47.5	407	6	US-10-953-349-2666	Sequence 2666, Ap
27	38	47.5	443	6	US-10-953-349-2665	Sequence 2665, Ap
28	37.5	46.9	630	7	US-11-293-697-3776	Sequence 3776, Ap
29	36	45.0	380	6	US-10-953-349-7175	Sequence 7175, Ap
30	36	45.0	391	6	US-10-953-349-7174	Sequence 7174, Ap
31	36	45.0	408	6	US-10-953-349-17120	Sequence 17120, A
32	36	45.0	442	6	US-10-953-349-7173	Sequence 7173, Ap
33	36	45.0	587	6	US-10-953-349-17119	Sequence 17119, A
34	36	45.0	674	6	US-10-953-349-17118	Sequence 17118, A
35	36	45.0	706	6	US-10-511-937-2450	Sequence 2450, Ap
36	35	43.8	307	6	US-10-953-349-2183	Sequence 2183, Ap
37	35	43.8	335	6	US-10-953-349-2182	Sequence 2182, Ap
38	35	43.8	343	6	US-10-953-349-2181	Sequence 2181, Ap
39	34	42.5	188	6	US-10-953-349-2975	Sequence 2975, Ap
40	34	42.5	206	6	US-10-953-349-7113	Sequence 7113, Ap
41	34	42.5	216	6	US-10-953-349-2974	Sequence 2974, Ap
42	34	42.5	244	6	US-10-953-349-7112	Sequence 7112, Ap
43	34	42.5	251	6	US-10-953-349-29525	Sequence 29525, A
44	34	42.5	255	6	US-10-953-349-7111	Sequence 7111, Ap
45	34	42.5	275	6	US-10-953-349-24596	Sequence 24596, A
46	34	42.5	298	6	US-10-953-349-24595	Sequence 24595, A
47	34	42.5	323	7	US-11-249-111-102	Sequence 102, App
48	34	42.5	345	6	US-10-511-937-2562	Sequence 2562, Ap
49	34	42.5	355	6	US-10-953-349-2973	Sequence 2973, Ap
50	34	42.5	398	6	US-10-953-349-20591	Sequence 20591, A
51	34	42.5	401	6	US-10-953-349-24594	Sequence 24594, A
52	34	42.5	415	6	US-10-953-349-20590	Sequence 20590, A
53	34	42.5	419	6	US-10-953-349-20589	Sequence 20589, A
54	34	42.5	580	6	US-10-953-349-24438	Sequence 24438, A
55	34	42.5	635	6	US-10-953-349-24437	Sequence 24437, A
56	34	42.5	636	6	US-10-953-349-24436	Sequence 24436, A
57	33	41.2	138	6	US-10-542-038-17	Sequence 17, Appl
58	33	41.2	159	6	US-10-542-038-4	Sequence 4, Appli
59	33	41.2	358	6	US-10-953-349-32194	Sequence 32194, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-7.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 7.rai.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:08:52; Search time 11.4238 Seconds

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-7

Perfect score: 81

Sequence: 1 YCEVPINFAMAALGG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents AA:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* 7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	81	100.0	399 399	_	US-09-553-498-2 US-09-618-869-2	Sequence 2, Appli Sequence 2, Appli

_				_		_	
3	77	95.1	380	2	US-09-543-681A-5912	Sequence	5912, Ap
4	77	95.1	380	2	US-09-489-039A-9011	Sequence	9011, Ap
5	68	84.0	381	2	US-09-252-991A-27174	Sequence	27174, A
6	59	72.8	376	3	US-10-375-010-22	•	22, Appl
7	57	70.4	209	2	US-09-902-540-14118	-	
				_			14118, A
8	45	55.6	288	2	US-09-107-532A-7120		7120, Ap
9	43	53.1	244	2	US-09-134-000C-4358	Sequence	4358, Ap
10	42	51.9	375	2	US-09-328-352-4984	Sequence	4984, Ap
11	42	51.9	417	2	US-09-489-039A-7357	Sequence	7357, Ap
12	41	50.6	274	2	US-09-248-796A-20766	_	20766, A
13	41	50.6	280	2	US-09-248-796A-20765		20765, A
14	41	50.6	648	2	US-09-538-092-536	_	536, App
15	39	48.1	127	2	US-09-198-452A-359		359, App
16	39	48.1	148	2	US-09-438-185A-344	Sequence	344, App
17	39	48.1	244	2	US-09-198-452A-360	Sequence	360, App
18	39	48.1	256	2	US-09-270-767-33692	-	33692, A
19	39	48.1	256	2	US-09-270-767-48909		48909, A
20	39	48.1	324	2	US-09-902-540-12246		
						_	12246, A
21	39	48.1	369	2	US-09-252-991A-18429	-	18429, A
22	39	48.1	370	2	US-09-377-285B-16	Sequence	16, Appl
23	39	48.1	370	2	US-10-192-381-16	Sequence	16, Appl
24	39	48.1	720	2	US-09-328-352-4435	Sequence	4435, Ap
25	39	48.1	1058	1	US-08-247-904B-14	-	14, Appl
26	39	48.1	1058	2	US-08-767-942A-15		15, Appl
				2	US-09-826-312A-2		
27	39	48.1	1058				2, Appli
28	39	48.1	1058	2	US-09-538-092-985		985, App
29	39	48.1	1058	3	US-10-835-096-2	Sequence	2, Appli
30	39	48.1	1059	2	US-09-542-497A-2	Sequence	2, Appli
31	39	48.1	1059	2	US-10-108-767-2	Seguence	2, Appli
32	39	48.1	1059	2	US-10-152-156-2		2, Appli
33	38	46.9	85	1	US-08-480-229C-7		7, Appli
34	38	46.9	85	1	US-08-659-235C-7		
							7, Appli
35	38	46.9	104	1	US-08-111-939-26		26, Appl
36	38	46.9	108	1	US-08-162-402B-27	_	27, Appl
37	38	46.9	318	2	US-09-902-540-15648	Sequence	15648, A
38	38	46.9	363	2	US-09-489-039A-13446	Sequence	13446, A
39	38	46.9	392	2	US-09-198-452A-48	Sequence	48, Appl
40	38	46.9	395	2	US-09-603-208A-28	_	28, Appl
41	38	46.9	406	2	US-09-438-185A-34	-	34, Appl
42		45.7		_			
	37		115	1	US-08-152-922A-7		7, Appli
43		45.7	158	2			35277, A
44	37	45.7	158	2	US-09-270-767-50494	_	50494, A
45	37	45.7	334	2	US-09-546-986A-8	Sequence	8, Appli
46	37	45.7	334	2	US-09-524-730-8	Sequence	8, Appli
47	37	45.7	427	2	US-09-489-039A-8493	Sequence	8493, Ap
48	37	45.7	502	2	US-09-134-000C-6611		6611, Ap
49	37	45.7	767	2	US-09-540-236-2346	_	2346, Ap
							2636, Ap
50	37	45.7	781	2	US-10-094-749-2636	-	_
51	37	45.7	861	2	US-09-949-016-11001		11001, A
52	37	45.7	1285	1	US-07-582-945-2		2, Appli
53	37	45.7	1285	1	US-08-453-141-2	Sequence	2, Appli
54	37	45.7	1285	2	US-08-293-314-2	Sequence	2, Appli
55	37	45.7	1602	2	US-09-269-874A-7	Sequence	7, Appli
56	37	45.7	1621	2	US-09-269-874A-5		5, Appli
57	37	45.7	1639	2	US-09-269-874A-3		3, Appli
58	36	44.4	183	2	US-09-252-991A-26190		26190, A
59	36	44.4	196	2	US-09-270-767-45964		45964, A
60	36	44.4	217	2	US-09-328-352-5479		5479, Ap
61	36	44.4	251	2	US-09-663-600A-99		99, Appl
62	36	44.4	251	2	US-09-663-600A-193	Sequence	193, App
63	36	44.4	358	2	US-09-134-001C-5461		5461, Ap
-	= *			_		<u>.</u>	·

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-7.ra

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-007. This page gives you Search Results detail for the Application 10001938 and Search Result us-10-007.

<u>start</u>

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:29:53; Search time 75.9934 Seconds

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-7

Perfect score: 81

Sequence: 1 YCEVPINFAMAALGG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ક				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	81	100.0	15	4	US-10-001-938-7	Sequence 7, Appli
2	81	100.0	161	5	US-10-450-763-55085	Sequence 55085, A
3	81	100.0	340	3	US-09-764-868-1153	Sequence 1153, Ap

				_		_	
4	81	100.0	341	3	US-09-764-868-1152	Sequence	1152, Ap
5	81	100.0	376	4	US-10-369-493-689	Sequence	689, App
6	81	100.0	376	6	US-11-080-458-32	Sequence	32, Appl
7	75	92.6	378	4	US-10-369-493-386	_	386, App
8	75	92.6	378	4	US-10-369-493-21305		21305, A
9	68	84.0	344	5	US-10-467-657-8284	_	8284, Ap
10	62	76.5	369	4	US-10-369-493-19646	Sequence	19646, A
11	60	74.1	374	4	US-10-369-493-13658	Sequence	13658, A
12	59	72.8	358	4	US-10-369-493-9641	-	9641, Ap
13	59	72.8	372	4	US-10-369-493-23206	_	23206, A
14				-			
	59	72.8	376	4	US-10-375-010-22	_	22, Appl
15	59	72.8	376	6	US-11-232-406A-22		22, Appl
16	59	72.8	378	4	US-10-369-493-8450	Sequence	8450, Ap
17	56	69.1	15	4	US-10-001-938-8	Sequence	8, Appli
18	56	69.1	376	4	US-10-369-493-12087	_	12087, A
19	54	66.7	382	4	US-10-369-493-8065		8065, Ap
				-		_	_
20	52	64.2	379	4	US-10-369-493-7330		7330, Ap
21	52	64.2	380	4	US-10-369-493-4573		4573, Ap
22	51	63.0	370	4	US-10-369-493-17209	Sequence	17209, A
23	51	63.0	384	6	US-11-074-176-78	Sequence	78, Appl
24	50	61.7	375	4	US-10-369-493-15859		15859, A
25	50	61.7	376	4		_	
				-	US-10-369-493-15487	_	15487, A
26	50	61.7	384	4	US-10-369-493-21849	-	21849, A
27	49	60.5	362	4	US-10-369-493-9305	Sequence	9305, Ap
28	46	56.8	377	6	US-11-045-004-1504	Sequence	1504, Ap
29	46	56.8	396	4	US-10-156-761-12020	Sequence	12020, A
30	45	55.6	376	4	US-10-369-493-1212	_	1212, Ap
31	45	55.6	467	4	US-10-074-978A-247	-	_
				-		-	247, App
32	44	54.3	364	6	US-11-087-099-10854	_	10854, A
33	43	53.1	152	4	US-10-767-701-51964	-	51964, A
34	43	53.1	271	5	US-10-506-454-953	Sequence	953, App
35	43	53.1	331	4	US-10-369-493-18770	Sequence	18770, A
36	43	53.1	385	4	US-10-369-493-16754	_	16754, A
37	42	51.9	123	3	US-09-764-877-1594	_	1594, Ap
38	42	51.9	123	4	US-10-242-515-1594	-	_
				_			1594, Ap
39	42	51.9	196	5	US-10-450-763-57058	_	57058, A
40	42	51.9	295	5	US-10-450-763-57057	Sequence	57057, A
41	42	51.9	403	5	US-10-732-923-23825	Sequence	23825, A
42	42	51.9	418	5	US-10-732-923-23808	Sequence	23808, A
43	42	51.9	418	5	US-10-732-923-23829		23829, A
44		51.9	428	5			48608, A
				_		_	
45	41	50.6	168	4	US-10-437-963-138551	Sequence	•
46	41	50.6	365	4	US-10-369-493-10648	_	10648, A
47	41	50.6	648	4	US-10-149-310-116	Sequence	116, App
48	41	50.6	759	4	US-10-149-310-218	Sequence	218, App
49	40	49.4	194	4	US-10-767-701-55799	Sequence	55799, A
50	40	49.4	241	6	US-11-188-298-6441		6441, Ap
51	40	49.4	330	4	US-10-369-493-19832	_	_
							19832, A
52	40	49.4	345	4	US-10-282-122A-74172	<u>-</u>	74172, A
53	40	49.4	345	4	US-10-474-776-387	_	387, App
54	40	49.4	345	5	US-10-472-928-4098	Sequence	4098, Ap
55	40	49.4	379	4	US-10-369-493-18523	Sequence	18523, A
56	40	49.4	413	5	US-10-732-923-23809		23809, A
57	39.5	48.8	416	6	US-11-188-298-349	_	349, App
58	39.5	48.8	1902		US-10-437-963-139559	_	
				4		Sequence	
59	39	48.1	110	4	US-10-425-115-265773	Sequence	
60	39	48.1	127	4	US-10-289-762-359	-	359, App
61	39	48.1	148	4	US-10-767-701-51826	Sequence	51826, A
62	39	48.1	166	4	US-10-424-599-181463	Sequence	
63	39	48.1	170	4	US-10-425-115-265740	Sequence	
64	39	48.1	205	5	US-10-450-763-53421		53421, A
			200	-		Sedacuce	33.21, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-7.rapbn.

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Comments / Suggestions

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-7.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title:

US-10-001-938-7

Perfect score: 81

1 YCEVPINFAMAALGG 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description	_
1	81	100.0	15	6	US-10-490-949-8	Sequence 8, Appl	i
2	56	69.1	15	6	US-10-490-949-9	Sequence 9, Appl	
3	43	53.1	389	7	US-11-122-986-185	Sequence 185, Ap	
4	43	53.1	389	7	US-11-122-986-187	Sequence 187, Ap	
5	39	48.1	177	6	US-10-953-349-40074	Sequence 40074,	-
6	39	48.1	1058	7	US-11-251-673-3	Sequence 3, Appl	
7	39	48.1	1058	7	US-11-328-747-2	Sequence 2, Appl	
8	38	46.9	264	6	US-10-953-349-31925	Sequence 31925,	A
9	38	46.9	299	6	US-10-953-349-31924	Sequence 31924,	Α
10	38	46.9	341	6	US-10-953-349-31923	Sequence 31923,	Α
11	36	44.4	337	6	US-10-953-349-34607	Sequence 34607,	Α
12	36	44.4	381	6	US-10-953-349-34606	Sequence 34606,	Α
13	35	43.2	20	7	US-11-301-554-1837	Sequence 1837, A	q.
14	35	43.2	20	7	US-11-301-554-1838	Sequence 1838, A	q.
15	35	43.2	200	7	US-11-301-554-324	Sequence 324, Ap	p
16	35	43.2	200	7	US-11-301-554-789	Sequence 789, Ap	
17	35	43.2	207	7	US-11-301-554-1667	Sequence 1667, A	
18	35	43.2	207	7	US-11-301-554-1913	Sequence 1913, A	_
19	35	43.2	468	6	US-10-953-349-13528	Sequence 13528,	
20	35	43.2	516	6	US-10-953-349-5638	Sequence 5638, A	
21	35	43.2	543	6	US-10-953-349-5637	Sequence 5637, A	
22	35	43.2	558	6	US-10-953-349-5636	Sequence 5636, A	
23	35	43.2	589	6	US-10-953-349-13527	Sequence 13527,	
24	35	43.2	620	6	US-10-953-349-13526	Sequence 13526,	Α
25	34.5	42.6	125	6	US-10-953-349-31810	Sequence 31810,	
26	34	42.0	134	6	US-10-953-349-25326	Sequence 25326,	
27	34	42.0	178	6	US-10-953-349-32321	Sequence 32321,	
28	34	42.0	188	6	US-10-953-349-32320	Sequence 32320,	
29	34	42.0	215	6	US-10-953-349-32319	Sequence 32319,	
30	34	42.0	269	6	US-10-953-349-35364	Sequence 35364,	
31	34	42.0	276	6	US-10-953-349-35363	Sequence 35363,	
32	34	42.0	279	6	US-10-953-349-35362	Sequence 35362,	
33	34	42.0	654	7	US-11-121-154-191	Sequence 191, Ap	
34	34	42.0	677	7	US-11-293-697-4521	Sequence 4521, A	
35	33	40.7	14	7	US-11-122-986-191	Sequence 191, Ap	-
36	33	40.7	236	6	US-10-953-349-2804	Sequence 2804, A	
37	33	40.7	241	6	US-10-953-349-23181	Sequence 23181,	
38	33	40.7	247	6	US-10-953-349-23180	Sequence 23180,	
39	33	40.7	337			Sequence 13157,	
40	33	40.7	387	6	US-10-953-349-13156	Sequence 13156,	
41	33	40.7	396	7	US-11-293-697-4386	Sequence 4386, A	_
42	33	40.7	423	6	US-10-953-349-2803	Sequence 2803, A	
43	33	40.7	425	6	US-10-953-349-15552	Sequence 15552, Sequence 2802, A	
44	33	40.7 40.7	429	6	US-10-953-349-2802	-	_
45 46	33 33	40.7	443 485	6 6	US-10-953-349-17462	Sequence 17462,	
47				7	US-10-953-349-13155	Sequence 13155,	
47	33 33	40.7 40.7	547 589		US-11-293-697-2751 US-11-311-778-6	Sequence 2751, A Sequence 6, Appl	
49	33	40.7	640	7 7		Sequence 4, Appl	
50	33	40.7	800	7	US-11-311-778-4 US-11-293-697-2490	Sequence 2490, A	
51	33	40.7	1178	7	US-11-311-778-10	Sequence 10, App	
52	33	40.7	1178	7	US-11-311-778-10 US-11-311-778-12	Sequence 12, App	
53	33	40.7	1178	7	US-11-311-778-14	Sequence 12, App	
54	32	39.5	252	6	US-10-953-349-8893	Sequence 8893, A	
55	32	39.5	253	6	US-10-953-349-8892	Sequence 8892, A	-
56	32	39.5	294	6	US-10-953-349-23218	Sequence 23218,	
57	32	39.5	302	6	US-10-953-349-8891	Sequence 8891, A	
58	32	39.5	312	6	US-10-953-349-23217	Sequence 23217,	
59	32	39.5	316	6	US-10-953-349-23216	Sequence 23216,	
				•			•

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-8.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 8.rai.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:12:07; Search time 12.7 Seconds

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-8

Perfect score: 74

Sequence: 1 PINFAMAALGGEIEV 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents AA:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1 2		100.0 100.0		_	US-09-553-498-2 US-09-618-869-2	Sequence 2, Appli Sequence 2, Appli

3	70	94.6	380	2	US-09-543-681A-5912	Sequence 5912, Ap
4	70	94.6	380	2	US-09-489-039A-9011	Sequence 9011, Ap
5	60	81.1	376	3	US-10-375-010-22	Sequence 22, Appl
6	59	79.7	381	2	US-09-252-991A-27174	Sequence 27174, A
7	47	63.5	209	2	US-09-902-540-14118	Sequence 14118, A
8	47	63.5	288	2	US-09-107-532A-7120	Sequence 7120, Ap
9	45	60.8	244	2	US-09-134-000C-4358	Sequence 4358, Ap
10	45	60.8	375	2	US-09-328-352-4984	Sequence 4984, Ap
				2		
11	44	59.5	407		US-09-540-236-2899	Sequence 2899, Ap
12	42	56.8	373	2	US-09-710-279-890	Sequence 890, App
13	42	56.8	385	2	US-09-134-001C-3688	Sequence 3688, Ap
14	42	56.8	395	2	US-09-603-208A-28	Sequence 28, Appl
15	41	55.4	274	2	US-09-248-796A-20766	Sequence 20766, A
16	41	55.4	280	2	US-09-248-796A-20765	Sequence 20765, A
17	40	54.1	253	2	US-08-975-762-52	Sequence 52, Appl
18	40	54.1	253	2	US-09-295-028-52	Sequence 52, Appl
19	40	54.1	253	2	US-09-106-582-52	Sequence 52, Appl
20	40	54.1	253	2	US-09-159-469-52	Sequence 52, Appl
21	40	54.1	253	2	US-09-693-542-52	Sequence 52, Appl
22	40	54.1	326	2	US-09-066-046-29	Sequence 29, Appl
23	40	54.1	326	2	US-09-066-047-15	Sequence 15, Appl
24	40	54.1	425	2	US-09-288-339-4	Sequence 4, Appli
25	40	54.1	435	2	US-09-066-046-27	Sequence 27, Appl
26	40	54.1	435	2	US-09-066-047-13	Sequence 13, Appl
27	39.5	53.4	538	2	US-09-107-532A-5563	Sequence 5563, Ap
28	39	52.7	324	2	US-09-902-540-12246	Sequence 12246, A
29	38	51.4	352	1	US-08-472-534-6	Sequence 6, Appli
30	38	51.4	378	2	US-09-583-110-4647	Sequence 4647, Ap
31	38	51.4	379	2	US-09-107-433-3487	Sequence 3487, Ap
		51.4	532	2	US-09-252-991A-21005	
32	38			_		Sequence 21005, A
33	37	50.0	34	1	US-08-118-270-190	Sequence 190, App
34	37	50.0	34	5	PCT-US93-08528-190	Sequence 190, App
35	37	50.0	127	2	US-09-198-452A-359	Sequence 359, App
36	37	50.0	148	2	US-09-438-185A-344	Sequence 344, App
37	37	50.0	244	2	US-09-198-452A-360	Sequence 360, App
38	37	50.0	321	2	US-09-498-520A-18	Sequence 18, Appl
39	37	50.0	394	2	US-09-252-991A-22328	Sequence 22328, A
40	37	50.0	413	1	US-08-282-197C-49	Sequence 49, Appl
41	37	50.0	1319	2	US-09-538-092-1291	Sequence 1291, Ap
42	37	50.0	1343	2	US-09-949-016-10641	Sequence 10641, A
43	36	48.6	35	_	US-08-118-270-191	Sequence 191, App
				1		
44	36	48.6	35	5	PCT-US93-08528-191	Sequence 191, App
45	36	48.6	82	2	US-09-144-776B-18	Sequence 18, Appl
46	36	48.6	82	2	US-08-882-431B-18	Sequence 18, Appl
47	36	48.6	121	2	US-09-252-991A-19703	Sequence 19703, A
48	36	48.6	199	2	US-10-360-101-216	Sequence 216, App
49	36	48.6	228	2	US-08-896-933-25	Sequence 25, Appl
50	36	48.6	228	2	US-09-314-235-25	Sequence 25, Appl
51	36	48.6	228	2	US-09-708-008B-25	Sequence 25, Appl
52	36	48.6	251	2	US-09-663-600A-99	Sequence 99, Appl
53	36	48.6	251	2	US-09-663-600A-193	Sequence 193, App
54	36	48.6	315	2	US-09-603-208A-212	Sequence 212, App
55	36	48.6	327	2	US-09-252-991A-28744	Sequence 28744, A
						——————————————————————————————————————
56	36	48.6	361	2	US-09-583-110-2683	Sequence 2683, Ap
57	36	48.6	363	2	US-09-107-433-3946	Sequence 3946, Ap
58	36	48.6	369	2	US-09-252-991A-18429	Sequence 18429, A
59	36	48.6	432	2	US-09-118-319-2	Sequence 2, Appli
60	36	48.6	464	2	US-09-252-991A-20795	Sequence 20795, A
61	36	48.6	473	2	US-09-252-991A-23441	Sequence 23441, A
62	36	48.6	483	2	US-09-603-208A-210	Sequence 210, App
63	36	48.6	657	2	US-09-252-991A-23156	Sequence 23156, A
				_		

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-8.ra

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 8.rapbm.

start

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OM protein - protein search, using sw model

June 2, 2006, 19:45:16; Search time 63.4 Seconds Run on:

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-8

Perfect score: 74

Sequence: 1 PINFAMAALGGEIEV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

2097797 segs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	74	100.0	15	4	US-10-001-938-8	Sequence 8, Appli
2	74	100.0	161	5	US-10-450-763-55085	Sequence 55085, A
3	74	100.0	340	3	US-09-764-868-1153	Sequence 1153, Ap

		100 0	0.41	_	00 564 060 1150		_
4	74	100.0	341	3	US-09-764-868-1152	Sequence 1152,	
5	74	100.0	376	4	US-10-369-493-689	Sequence 689,	App
6	74	100.0	376	6	US-11-080-458-32	Sequence 32, A	ppl
7	68	91.9	378	4	US-10-369-493-386	Sequence 386,	
8	68	91.9	378	4	US-10-369-493-21305	Sequence 21305	
9	67	90.5	344	5	US-10-467-657-8284	Sequence 8284,	
						•	-
10	61	82.4	369	4	US-10-369-493-19646	Sequence 19646	
11	60	81.1	376	4	US-10-375-010-22	Sequence 22, A	ppl
12	60	81.1	376	6	US-11-232-406A-22	Sequence 22, A	ppl
13	60	81.1	378	4	US-10-369-493-8450	Sequence 8450,	ДÞ
14	58	78.4	365	4	US-10-369-493-10648	Sequence 10648	-
15	56	75.7	15	4	US-10-001-938-7	Sequence 7, Ap	
16	56	75.7	379		US-10-369-493-7330	-	_
				4		Sequence 7330,	
17	56	75.7	380	4	US-10-369-493-4573	Sequence 4573,	_
18	55	74.3	382	4	US-10-369-493-8065	Sequence 8065,	Аp
19	55	74.3	396	4	US-10-156-761-12020	Sequence 12020	, A
20	54	73.0	374	4	US-10-369-493-13658	Sequence 13658	, A
21	53	71.6	372	4	US-10-369-493-23206	Sequence 23206	
22	51	68.9	384	4	US-10-369-493-21849	Sequence 21849	
23	50	67.6	379	4		Sequence 18523	
				-	US-10-369-493-18523		
24	49	66.2	365	4	US-10-369-493-18240	Sequence 18240	
25	48	64.9	358	4	US-10-369-493-9641	Sequence 9641,	Аp
26	47	63.5	384	6	US-11-074-176-78	Sequence 78, A	ppl
27	47	63.5	420	4	US-10-369-493-591	Sequence 591,	App
28	46	62.2	370	4	US-10-369-493-17209	Sequence 17209	
29	46	62.2	376	4	US-10-369-493-1212	Sequence 1212,	
30	45	60.8	377	6	US-11-045-004-1504	_	
						Sequence 1504,	
31	44	59.5	354	4	US-10-369-493-11087	Sequence 11087	
32	44	59.5	376	4	US-10-369-493-12087	Sequence 12087	
33	43.5	58.8	271	5	US-10-506-454-953	Sequence 953,	App
34	43	58.1	256	4	US-10-424-599-248436	Sequence 24843	6,
35	43	58.1	274	4	US-10-425-115-253738	Sequence 25373	
36	43	58.1	1316	4	US-10-437-963-143011	Sequence 14301	
37	42	56.8	114	4	US-10-437-963-113572	Sequence 11357	
38	42	56.8	118	4	US-10-424-599-195865	<u>-</u>	
						Sequence 19586	
39	42	56.8	365	4	US-10-369-493-13503	Sequence 13503	
40	42	56.8	373	5	US-10-793-626-890	Sequence 890,	
41	42	56.8	385	4	US-10-369-493-16754	Sequence 16754	, A
42	42	56.8	395	3	US-09-738-626-6574	Sequence 6574,	Аp
43	42	56.8	395	5	US-10-703-799B-28	Sequence 28, A	ppl
44	42	56.8	665	6	US-11-097-143-19728	Sequence 19728	
45	41	55.4	398	6	US-11-098-686-11398	Sequence 11398	
46	40	54.1	177	4	US-10-425-114-39492	Sequence 39492	-
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47	40	54.1	253	3	US-09-159-469-52	Sequence 52, A	
48	40	54.1	253	3	US-09-798-042-52	Sequence 52, A	
49	40	54.1	253	3	US-09-953-108-52	Sequence 52, A	
50	40	54.1	330	5	US-10-732-923-13089	Sequence 13089	, A
51	40	54.1	424	4	US-10-437-963-192231	Sequence 19223	1,
52	40	54.1	425	4	US-10-223-598-4	Sequence 4, Ap	
53	40	54.1	587	4	US-10-425-114-73019	Sequence 73019	_
54	40	54.1	724	4	US-10-437-963-121905	Sequence 12190	
						-	
55	39.5	53.4	519	4	US-10-282-122A-57987	Sequence 57987	
56	39	52.7	163	4	US-10-437-963-196051	Sequence 19605	
57	39	52.7	385	5	US-10-501-282-4398	Sequence 4398,	_
58	39	52.7	395	6	US-11-079-463-9803	Sequence 9803,	Аp
59	39	52.7	471	4	US-10-369-493-5554	Sequence 5554,	Аp
60	39	52.7	471	4	US-10-369-493-5555	Sequence 5555,	
61	38	51.4	142	4	US-10-767-701-39309	Sequence 39309	_
62	38	51.4	208	4			
					US-10-425-114-67304	Sequence 67304	
63	38	51.4	238	4	US-10-156-761-9379	Sequence 9379,	
64	38	51.4	239	4	US-10-425-115-270985	Sequence 27098	ο,

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-8.rapbn.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-8.rapbn.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-8

Perfect score: 74

Sequence:

1 PINFAMAALGGEIEV 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description
1	74	100.0	15	6	US-10-490-949-9	Sequence 9, Appli
2	56	75.7	15	6	US-10-490-949-8	Sequence 8, Appli
3	45	60.8	389	7	US-11-122-986-185	Sequence 185, App
4	45	60.8	389	7	US-11-122-986-187	Sequence 187, App
5	37	50.0	467	6	US-10-953-349-32451	Sequence 32451, A
6	37	50.0	519	6	US-10-953-349-32450	Sequence 32450, A
7	37	50.0	521	6	US-10-953-349-32449	Sequence 32449, A
8	36	48.6	201	6	US-10-953-349-34141	Sequence 34141, A
9	36	48.6	207	6	US-10-953-349-34140	Sequence 34140, A
10	36	48.6	260	6	US-10-953-349-34139	Sequence 34139, A
11	35	47.3	368	6	US-10-953-349-7589	Sequence 7589, Ap
12	35	47.3	391	6	US-10-953-349-7588	Sequence 7588, Ap
13	35	47.3	438	6	US-10-953-349-7587	Sequence 7587, Ap
14	35	47.3	516	6	US-10-953-349-5638	Sequence 5638, Ap
15	35	47.3	543	6	US-10-953-349-5637	Sequence 5637, Ap
16	35	47.3	558	6	US-10-953-349-5636	Sequence 5636, Ap
17	34.5	46.6	312	7	US-11-140-450-81	Sequence 81, Appl
18	34	45.9	112	6	US-10-953-349-7574	Sequence 7574, Ap
19	34	45.9	249	6	US-10-953-349-14125	Sequence 14125, A
20	34	45.9	266	6	US-10-953-349-14124	Sequence 14124, A
21	34	45.9	382	6	US-10-953-349-14123	Sequence 14123, A
22	34	45.9	396	7	US-11-293-697-4386	Sequence 4386, Ap
23	34	45.9	677	7	US-11-293-697-4521	Sequence 4521, Ap
24	34	45.9	1049	7	US-11-251-340-23	Sequence 23, Appl
25	34	45.9	1058	7 7	US-11-251-673-3	Sequence 3, Appli
26	34	45.9	1058 193	7	US-11-328-747-2 US-11-301-951-2	Sequence 2, Appli
27 28	33 33	44.6 44.6	193	7	US-11-301-951-2 US-11-301-951-4	Sequence 2, Appli Sequence 4, Appli
29	33	44.6	193	7	US-11-301-951-6	Sequence 6, Appli
30	33	44.6	193	7	US-11-301-951-8	Sequence 8, Appli
31	33	44.6	217	6	US-10-953-349-18535	Sequence 18535, A
32	33	44.6	283	6	US-10-953-349-18534	Sequence 18534, A
33	33	44.6	307	6	US-10-953-349-18533	Sequence 18533, A
34	33	44.6	335	6	US-10-953-349-13374	Sequence 13374, A
35	33	44.6	339	6	US-10-953-349-13373	Sequence 13373, A
36	33	44.6	348	6	US-10-953-349-13372	Sequence 13372, A
37	33	44.6	425	6	US-10-953-349-15552	Sequence 15552, A
38	33	44.6	544	6	US-10-953-349-28426	Sequence 28426, A
39	33	44.6	788	7	US-11-121-154-47	Sequence 47, Appl
40	33	44.6	1912	6	US-10-511-937-2561	Sequence 2561, Ap
41	32.5	43.9	654	7	US-11-121-154-191	Sequence 191, App
42	32	43.2	122	6	US-10-953-349-5458	Sequence 5458, Ap
43	32	43.2	161	6	US-10-953-349-33744	Sequence 33744, A
44	32	43.2	174	6	US-10-953-349-5457	Sequence 5457, Ap
45	32	43.2	174	6	US-10-953-349-39794	Sequence 39794, A
46	32	43.2	278	6	US-10-953-349-30456	Sequence 30456, A
47	32	43.2	302	7	US-11-293-697-2615	Sequence 2615, Ap
48	32	43.2	350	6	US-10-522-043-8	Sequence 8, Appli
49	32	43.2		6	US-10-199-229-14	Sequence 14, Appl
50	32	43.2	875	6	US-10-199-229-10	Sequence 10, Appl
51	32	43.2	951	6	US-10-199-229-9	Sequence 9, Appli
52 53	32	43.2	951	6	US-10-199-229-13	Sequence 13, Appl
53 54	32 31.5	43.2			US-10-505-928-325 US-11-293-697-2786	Sequence 325, App Sequence 2786, Ap
54 55	31.5	42.6 41.9		6	US-11-293-697-2766 US-10-953-349-37272	Sequence 37272, A
56	31	41.9		6	US-10-953-349-37272 US-10-953-349-29145	Sequence 29145, A
57	31	41.9	182	6	US-10-953-349-29145	Sequence 1326, Ap
58	31	41.9	189	6	US-10-953-349-25147	Sequence 25147, A
59	31	41.9	206		US-10-953-349-1325	Sequence 1325, Ap
	51		200	•	13 10 100 010 1020	4mones 1010, ub

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-9.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 9.rai.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:37:25; Search time 14.6053 Seconds Run on:

(without alignments)

89.896 Million cell updates/sec

Title: US-10-001-938-9

Perfect score: 73

Sequence: 1 ASYYEILDVPRSASA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:* 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1 73 100.0 277 1 US-08-868-288A-7 Sequence 7 2 73 100.0 277 2 US-09-235-373-7 Sequence 7	

_				_		
3	73	100.0	277	2	US-09-388-993-7	Sequence 7, Appli
4	73	100.0	277	2	US-09-501-714-7	Sequence 7, Appli
5	73	100.0	327	2	US-09-949-016-11262	Sequence 11262, A
6	73	100.0	351	1	US-08-868-288A-6	Sequence 6, Appli
7	73	100.0	351	2	US-09-235-373-6	Sequence 6, Appli
8	73	100.0	351	2	US-09-388-993-6	Sequence 6, Appli
9	73	100.0	351	2	US-09-501-714-6	Sequence 6, Appli
10	52	71.2	96	2	US-09-621-976-4045	Sequence 4045, Ap
11	52	71.2	223	2	US-09-658-644-4	Sequence 4, Appli
12	52	71.2	223	2	US-09-949-016-6832	Sequence 6832, Ap
13	52	71.2	267	2	US-09-949-016-11497	Sequence 11497, A
14	51	69.9	419	1	US-08-686-417-3	Sequence 3, Appli
15	48	65.8	286	2	US-09-248-796A-16992	Sequence 16992, A
16	48	65.8	387	2	US-09-908-992B-11	-
						Sequence 11, Appl
17	48	65.8	414	2	US-09-908-992B-10	Sequence 10, Appl
18	48	65.8	452	2	US-09-908-992B-29	Sequence 29, Appl
19	48	65.8	453	2	US-09-908-992B-9	Sequence 9, Appli
20	48	65.8	453	2	US-09-908-992B-30	Sequence 30, Appl
21	48	65.8	479	2	US-09-908-992B-28	Sequence 28, Appl
22	48	65.8	480	2	US-09-908-992B-8	Sequence 8, Appli
23	48	65.8	480	2	US-09-908-992B-12	Sequence 12, Appl
24	46	63.0	358	1	US-08-868-288A-1	Sequence 1, Appli
25	46	63.0	358	2	US-09-235-373-1	Sequence 1, Appli
26	46	63.0	358	2	US-09-388-993-1	Sequence 1, Appli
27	46	63.0	358	2	US-09-991-181-148	Sequence 148, App
28	46	63.0	358	2	US-09-501-714-1	Sequence 1, Appli
29	46	63.0	358	2	US-09-990-444-148	Sequence 148, App
30	46	63.0	358	2	US-09-997-333-148	Sequence 148, App
31	46	63.0	358	2	US-09-992-598-148	Sequence 148, App
32	46	63.0	358	2	US-09-989-735-148	
						Sequence 148, App
33	46	63.0	358	3	US-09-989-726-148	Sequence 148, App
34	46	63.0	358	3	US-09-997-514-148	Sequence 148, App
35	46	63.0	358	3	US-09-989-728-148	Sequence 148, App
36	46	63.0	358	3	US-09-997-349-148	Sequence 148, App
37	46	63.0	358	3	US-09-997-653-148	Sequence 148, App
38	46	63.0	358	3	US-09-989-293A-148	Sequence 148, App
39	44	60.3	311	2	US-09-248-796A-16958	Sequence 16958, A
40	43	58.9	147	2	US-09-513-999C-6925	Sequence 6925, Ap
41	42	57.5	138	2	US-09-902-540-13689	Sequence 13689, A
42	42	57.5	276	2	US-09-270-767-43364	Sequence 43364, A
43	42	57.5	391	2	US-09-902-540-11110	Sequence 11110, A
44	41	56.2	254	2	US-09-859-822-2	Sequence 2, Appli
45	41	56.2	373	2	US-09-710-279-890	Sequence 890, App
46	41	56.2	385	2	US-09-134-001C-3688	Sequence 3688, Ap
47	41	56.2	514	2	US-09-252-991A-18326	Sequence 18326, A
48	40	54.8	95	2	US-09-248-796A-19797	Sequence 19797, A
49	40	54.8	145	2	US-09-427-700-9	Sequence 9, Appli
50	40	54.8	146	1	US-07-989-363-2	Sequence 2, Appli
51	40	54.8	146	1	US-08-264-526-2	Sequence 2, Appli
52	40	54.8	320	2	US-09-328-352-7937	Sequence 7937, Ap
53 54	40	54.8	330	1	US-08-868-288A-3	Sequence 3, Appli
54	40	54.8	330	2	US-09-235-373-3	Sequence 3, Appli
55 56	40	54.8	330	2	US-09-388-993-3	Sequence 3, Appli
56	40	54.8	330	2	US-09-501-714-3	Sequence 3, Appli
57	40	54.8	376	3	US-10-375-010-22	Sequence 22, Appl
58	40	54.8	422	1	US-08-152-483B-3	Sequence 3, Appli
59	40	54.8	426	1	US-08-152-483B-7	Sequence 7, Appli
60	40	54.8	478	1	US-08-152-483B-9	Sequence 9, Appli
61	40	54.8	497	2	US-09-328-352-7286	Sequence 7286, Ap
62	40	54.8	503	2	US-09-562-737-68	Sequence 68, Appl
63	39	53.4	43	2	US-09-209-676-77	Sequence 77, Appl

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-9.rapbm.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:58:51; Search time 63.3553 Seconds

(without alignments)

109.671 Million cell updates/sec

Title:

US-10-001-938-9

Perfect score: 73

Sequence: 1 ASYYEILDVPRSASA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters:

2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA Main:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:* 5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ક

Result Query

No. Score Match Length DB ID

Description

1	73	100.0	15	4	US-10-001-938-9	Sequence 9, Appli
1 2	52		223	4	US-10-028-072-30	
		71.2				Sequence 30, Appl
3	52	71.2	223	4	US-10-140-808-30	Sequence 30, Appl
4	52	71.2	223	4	US-10-121-049-30	Sequence 30, Appl
5	52	71.2	223	4	US-10-123-904-30	Sequence 30, Appl
6	52	71.2	223	4	US-10-140-470-30	Sequence 30, Appl
7	52	71.2	223	4	US-10-175-746-30	Sequence 30, Appl
8	52	71.2	223	4	US-10-176-918-30	Sequence 30, Appl
9	52	71.2	223	4	US-10-176-921-30	Sequence 30, Appl
10	52	71.2	223	4	US-10-137-865-30	Sequence 30, Appl
11	52	71.2	223	4	US-10-140-474-30	Sequence 30, Appl
12	52	71.2	223	4	US-10-142-431-30	Sequence 30, Appl
13	52	71.2	223	4	US-10-143-114-30	Sequence 30, Appl
14	52	71.2	223	4	US-10-142-419-30	Sequence 30, Appl
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43	52	71.2	223	4	US-10-131-830A-30	Sequence 30, Appl
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1 ASYYEILDVPRSASA 15 Sequence:

Scoring table: BLOSUM62

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58871 seqs, 11565156 residues Searched:

58871 Total number of hits satisfying chosen parameters:

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> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:* 3: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:* 4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

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SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description	on
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2	51	69.9	161	6	US-10-953-349-37092	_	37092, A
3	51	69.9	190	6	US-10-953-349-37091	Sequence	37091, A
4	41	56.2	419	6	US-10-953-349-1054	Sequence	1054, Ap
5	40	54.8	417	6	US-10-953-349-16377	Sequence	16377, A
6	39	53.4	160	6	US-10-953-349-6860	Sequence	6860, Ap
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9	37	50.7	158	6	US-10-953-349-20727		20727, A
10	37	50.7	159	6	US-10-953-349-20726	-	20726, A
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54	34	46.6	250	6	US-10-953-349-39890	_	39890, A
55	34	46.6	253	6	US-10-953-349-5910	-	5910, Ap
56	34	46.6	255	6	US-10-953-349-9313		9313, Ap
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